STIC-Biotech/ChemLib

146933

From:

مشد و ۱۹۰۵ م

Hamud, Fozia

Sent:

Thursday, March 03, 2005 3:29 PM

To:

STIC-Biotech/ChemLib

Subject:

sequence search for 09/617,720

Please search SEQ ID NOs: 1, 2, 3 of 09/617,720 against commercial and interference data bases. thanks.

Fozia Hamud
Patent Examiner
Remsen 4D64
Mail Box: Remsen 4C70
(571) 272-0884

STAFF USE OI	NLY
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Type of Search

NA Sequence: #______

AA Sequence :#______

Structure: #______

Bibliographic:

Litigation:

Patent Family:

Other:

Vendors and cost where applicable STN:______
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____

Other(Specify):__

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March 13, 2005, 11:56:15; Search time 137.39 Seconds (without alignments) 11636.250 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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44446666666666666666666666666666666666		B1090567 602855674F1 NIH_MGC_10 Homo manna sequence. B1090567.1 G1:14508897 BEST. Homo sapiens (human) National Institutes of Heali Unpublished (1999) Contact: Robert Strausberg, Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Incond Library Arrayed by: Incyte of CDNA Library Parayed by: Incyte of CDNA Library Parayed by: Incyte of CDNA Library Arrayed by: Incyte of COT of	ch 1 Similarity 42; Conserv
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AL545100 LOCUS DEFINITION

RESULT 2

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 BVRV cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitogen.
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SEAUMC007944 Sea urchin primary mesenchyme cell cDNA library
Strongylocentrotus purpuratus cDNA clone PM990802-04-0459 5', mRNA
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Zhu,X., Mahairas,G., Illies,M.R., Cameron,R.A., Davidson,E.H. and
Ettensohn,C.A.
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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/plasmid="pcMvSPORT_6"
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/cell_type="primary mesenchyme_cells"
/lab_host="E.coli"
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Dept. Biol. Sci.
Carnegie Mellon University
Tel: +1 412 268 5849
Email: ettensohn@andrew.cmu.edu.
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Development 128 (13), 2615-2627 (2001)
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/db_xref="taxon:7668"
/clone="PM990802-04-0459"
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope - Centrer National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Bmail: sequencope.cns.fr, Web : www.sacope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMYSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2605 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CSODI013YA07 of Placenta Cot 25-normalized of Homo sapiens (human).
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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AL545100 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI013YA07 5-PRIME, mRNA sequence.
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1. (bases 1 to 2605)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 985)
Li, Wa.B., Gruber, C., Gessee, J. and Polayes, D. Full-length cDNA libraries and normalization Dmbblished (2001)
On Feb 15, 2001 this sequence version replaced gi:31266936.
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     31 AAGGAAGGAGGAAAGGAAGGAGTGAAGGAAGGAAGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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HTC; CNSLT_CDNA.
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FEATURES

Best Local Matches 4

8 셤

DRIGIN

ORGANISM

TITLE JOURNAL REMARK

AUTHORS

REFERENCE

DEFINITION

RESULT 3 CR613851

ACCESSION

VERSION KEYWORDS

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VERSION KEYWORDS

ઠ 셤 SOURCE

TITLE

COMMENT

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/clone lib="NCI CGAP Oy32"
/note="Organ: ovary; Vector: pAMP1; mRNA made from ovarian
cardinoma, cDNA made by oligo-dr prining
Non-directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Non-amplified library. "
                                                                                                                                                                                                                                                                                                                   AI252833 102_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1984923 3',
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 154)
Zhao,S., Niezman,W., Feldblyum,T., Malek,J., Shatsman,S.,
Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Frasner,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 103)

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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)
                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 bp DNA linear G
RPCI-23-385H23.TV RPCI-23 Mus musculus genomic clone
RPCI-23-385H23, genomic survey sequence.
AZ022385
                                                 Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="papillary serous carcinoma"
/lab_host="DH10B"
                                                                                                  Indela
                                                                                                                                               42
                                                                                                                                                                                           104 AGGATGGAGGTAGAAAGGAAGGAAGGAAGGAAGGAGTGAGA 64
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                                                                                                                                               2 AGGAAGGAGGAAAGGAAAGGAGTGAAGGAAGGAGGAGTGAAA
                                              78.6%; Score 33; DB 8;
87.8%; Pred. No. 16;
iive 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1984923"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
unknown library type
Seg primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                           AI252833.1 GI:3849362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                            Query Match
Best Local Similarity 87.89
....nhes 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Matches 35; Conserv
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AZ022385/c
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AUTHORS
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SOURCE
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AI252833
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalot (gilly 4732114|gb|AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                        GSS 14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 108, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 643)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longaren, S., Mahmoud, M., Meenen, E., Pedersen, T., Niederhauseern, A. and Wright, D., Weise, R., Tingey, A., von Niederhauseern, A. and Wright, D., Weise, R.
                                                                                                                                                                                                                                                                                                                     AZ649302 643 bp DNA linear GSS 14-DEC-200
1M0518F16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0518F16 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                Gaps
                                                                                                  ö
                                            82.4%; Score 34.6; DB 4; Length 818; 90.2%; Pred. No. 5.8; tive 0; Mismatches 4; Indels (
                                                                                                                                                                                           1 AAGGAAGGAGGAAGGAAGGAAGGAAGGAAGGAGGAGTGAA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0518 row: F column: 16
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Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 643.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="UUGC1M0518F16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                        AZ649302.1 GI:11782476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: plasmid ends
                                            Query Match 3
Best Local Similarity 90.29
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 643
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FEATURES

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Mus musculus (house mouse)
Mus musculus
        Email: ekirknes@tigr.org
Class: shotgun.
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GSS.
                                                                   j. .156
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AZ714952/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-23"
//note="Organ: Kidney/Brain; Vector: pBAC63.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBAC63.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
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The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838.0208
Fax: 301-838-0208
                                                                                                                                                                                            Email: szhao@tigr.org

Clones are derived from the mouse BAC.library RPCI-23. For BAC
library availability, please contact Piecer de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq prime: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis familiaris (dog)
Canis familiaris (dog)
Canis familiaris
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 156)
1 (kixness, E.P., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ligr-gss-dog-17000371107331 Dog Library Canis familiaris genomic, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                         Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAGGAAGGAGAAAGGAAAGGAGTGAAGGAAGGAGTGAA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AAGGAAGGAGGAGGAAGGAAGGAAGGAAGGAA 21
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-385H23.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="RPCI-23-385H23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
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                                                                     Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.4
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            Class: BAC ends.
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CE100567
LOCUS
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Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
Rejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 122 row: O column: 14
Seq primer: SP6
Class: BAC ends.
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/clone_lib="RPCI-24"
/note=Tvector: pTARBAC1; Site 1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Mussell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other GSSs RPCI-24-122014.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
Tyll Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 161)
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                            /organism="Canis familiaris"
/mol type="genomic DNA"
/strain="Standard Poodle"
/db xref="texon:9615"
/clon=lib="Dog Library"
/note="Site 1: BetXI; Libraries were prepared from peripheral Dlood"
                                                                                                                                                                                                                                                                                                                                                                                                         ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 bp DNA linear ( RPCI-24-122014.TJ RPCI-24 Mus musculus genomic clone RPCI-24-122014, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                            Length 156
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                      Query Match 74.8%; Score 31.4; DB 9;
Best Local Similarity 85.4%; Pred. No. 39;
Matches 35; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l. .161
'organism="Mus musculus"
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'clone="RPCI-24-122014"
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'strain="C57BL/6J"
Location/Qualifiers
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GSS 21-FEB-2001

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/sex="Male" | Jeach | 
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 346)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Niederhausern, A. and Wright, D., Weise, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                              AZ868613 346 bp DNA linear GSS 21-FEB-200
2M0180H20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                              clone UUGC2M0180H20 F, genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 10000 Std Error: Plate: 0180 row: H column: 20 Seg primer: CGTFGTAAAACGACGGCCAGT Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 346.
Location/Qualifiers
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/strain="C57BL/6J"
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/clone="UUGC2M0180H20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                              Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                 AZ868613.1 GI:13072103
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84112, USA
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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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                                                                                                                                                                                                                                                                                                                                                          AQ980187
RPCI-23-342A9.TV RPCI-23 Mus musculus genomic clone RPCI-23-342A9,
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Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

Clones are derived from the mouse BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 372 row: A column: 9

Seq primer: 77

Class: BAC ends.
                                                                   Gaps
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   Length 161;
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                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Other GSSs: RPCI-23-342A9.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Conter Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                   Indels
                                                                                                                                   41
                                                                                                                                                                                         102 AAGGAAGAAGGAAGGAAGGAAAGAAAAGGAATGAA 62
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   DB 8;
Query Match 74.8%; Score.31.4; D
Best Local Similarity 85.4%; Pred. No. 39;
Matches 35; Conservative 0; Mismatches
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/mol type="@encmic niv."
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/strain="C57BL/6J"
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/clone="RPCI-23-342A9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence.
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Std Error: 0.00

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74.8%; Score 31.4; DB 8; Length 346; larity 85.4%; Pred. No. 43; Conservative 0; Mismatches 6; Indels (
                                                                                          1 AAGGAAGGAGGAGAAGGAAGGAGGAAGGAAGGAGTGAA 41
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106 AAGGAAGGAGGAGGAAGGAAGGAAGGAAGGAAGGAA 66

RESULT 11

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4Q628256/c

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 514)
Marra, M.; Hillier, J., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                        Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:567719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vm69d08.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:1003503 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 424;
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                                                                                                                                                                                                              Seg primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 423.
Location/Qualifiers
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Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
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clone="IMAGE:1196437"
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Location/Qualifiers
1..514
    WashU-HHMI Mouse EST Project
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/strain="C57BL/6"
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A08 bp DNA linear GSS 16-JUN-1999 CITBL-E1-2650L1.TR CITBL-E1 Homo sapiens genomic clone 2650L1, A6202.2
                                                                                                                                                                                                                                                                          Zhao,S., Adame,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV.94173
VUG7D67.rl Stratagene mouse skin (#937313) Mus musculus CDNA clone
AAV.94417196437 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                    Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building
Unpublished (1997)
Other GSSs: CITBI-E1-2650L1.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moors,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
and search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell type="sperm"
/clone_lib="CITBI-E1"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 AAGGAAGGAGGGGGGAAGGAAGGAAGGAAGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 31.4; DB
; Pred. No. 43;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .408
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/mol_type="genomic DNA"
/db &ref="taxon:9606"
/clone="2650L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                       AQ628256
AQ628256.1 GI:5090648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA794173.1 GI:2857128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.8%;
                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                         (bases 1 to 408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.49
Matches 35; Conservative
                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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DEFINITION

AA794173 LOCUS

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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Gaps .,

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 524)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amcunts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF898116 524 bp mRNA linear EST 04-NOV-2003 A0234D08-5 NIA Mouse Embryonic Germ Cell cDNA Library (Long, subtracted) Mus musculus cDNA clone NIA:A0234D08 IMAGE:30731659 5',
                                                                                                                                                               /clone_lib="NIA Mouse Embryonic Germ Cell cDNA Library (Long, subtracted)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site_l: Sall;
Site_2: Not!, Mouse CDNA project by the Laboratory of GeneTics, National Institute on Aging (NIA), Intramural
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Sulte 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: A0234 row: D column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                               ch 74.8%; Score 31.4; DB 1; Length 514; l Similarity 85.4%; Pred. No. 45; 35; Conservative 0; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 AAGGAAGGAGGAAGGAAGGAAGGAAGGAAGGAAGGAA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="niaEST:A0234D08-5"
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/clone="NIA:A0234D08 IMAGE:30731659"
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/lab_host="DH108"
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/organism="Mus musculus"
musculus"
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Seg primer: M13 Reverse
High quality sequence stop: 524
                                                                                    /clone="IMAGE:1003503"
                                                              /db_xref="taxon:10090
                                                                                                   /tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="C57BL6"
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CF898116
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Mus musculus
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Best Local Similarity
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LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
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pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2kb. The library was constructed by Yulan Piao and Kazuhiro

ORIGIN

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Gaps . 0 74.8%; Score 31.4; DB 7; Length 524; 85.4%; Pred. No. 45; ive 0; Mismatches 6; Indels C 1 AAGGAAGGAGGAAGGAAGGAAGGAAGGAAGGAAGTGAA 41 Best Local Similarity 85.4 Matches 35; Conservative Query Match ò

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Search completed: March 13, 2005, 18:14:03 Job time : 144.39 secs

1. Sequence 1, Appli Sequence 102, App Sequence 11835, A Sequence 11835, A Sequence 11836, A Sequence 11926, A Sequence 11934, A Sequence 11934, A Sequence 11934, A Sequence 115921, A Sequence 1250, A Sequence 1250, A Sequence 13312, A Sequence 1312, A Sequence 1312, A Sequence 1312, A Sequence 1312, A

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301 GIGCCAAGGAAICCAAGAGCIICACCIICIACCGGCGGGACAIGGGGCICACCICCAGCI 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 AGGGGAGTCTACACCCTGTGGAGCTCAAGATGGTCCTGAGTGGGGCGCTGTGCTTCCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 TGAAGGACTCGGCATTGAAGGTGCTTTATCTGCATAATAACCAGCTTCTAGCTGGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCATGCAGGGAAGGTCATTAAAGGTGAAGATCAGCGTGGTCCCCAATCGGTGGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REPERBACE: CLOO1307 CURRENT APPLICATION NUMBER: US/09/949,016 CURRENT FILING DATE: 2000-04-14 PRIOR FILING DATE: 2000-10-20 PRIOR FILING DATE: 2000-10-03 PRIOR APPLICATION NUMBER: 60/231,768 PRIOR PRILING DATE: 2000-10-03 PRIOR PRILING DATE: 2000-10-03 PRIOR PRILING DATE: 2000-09-08 PRIOR FILING DATE: 2000-09-09 PRIOR FILING DATE: 2000-09-09 PRIOR FILING DATE: 2000-09-09 PRIOR FILING DATE: 2000-09-09 PRIOR FILING
                                                               US-09-573 080A-102
US-09-949-016-15868
US-09-949-016-11835
US-09-949-016-11835
US-09-949-016-11926
US-09-949-016-11926
US-09-949-016-11934
US-09-949-016-15501
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-949-016-3485, Application US/09949016; Patent No. 6812339; GENERAL INFORMATION:
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99.6%;
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Best Local Similarity 99.6
Matches 2553; Conservative
11.1 357
11.1 357
17.7 466
6.1 374159
6.0 100550
6.0 100550
5.8 21456
5.8 21456
5.8 21456
5.8 2266293
5.7 124480
5.4 64047
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4. 4. 4. 4.
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ORGANISM: Human
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Sequence 12698, A
Sequence 15227, A
Sequence 8, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 6, Appli
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Sequence 6, Appli
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Sequence 6, Appli
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                                                                                                                                                       ; Search time 478.866 Seconds
(without alignments)
8757.724 Million cell updates/sec
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*
(cgn2_6/ptodata/1/ina/5B_COMB.seq:*
(cgn2_6/ptodata/1/ina/6A_COMB.seq:*
(cgn2_6/ptodata/1/ina/6B_COMB.seq:*
(cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
(cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-417-455-6

US-09-348-94-6

US-09-547-626-6

US-09-949-016-12698

US-09-949-016-12698

US-09-949-016-12698

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US-09-457-626-8

US-09-457-626-8

US-09-457-626-8

US-09-477-626-7

US-09-477-626-7

US-09-477-626-4

US-09-477-626-2

US-09-477-626-2

US-09-49-016-36644

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-09-949-016-123784
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US-09-417-455-6
Sequence 6, Application US/09417455
patent No. 629465
; Sequence 6, Application US/09417455
; Patent No. 629465
; GENERAL INPORMATION:
APPLICANT: Ford, John
TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECI
FILE REFERENCE: 28110/36328
; CURRENT FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US/09/417,455
; CURRENT FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 09/281,210
; PRIOR PILING DATE: 1999-04-05
; PRIOR PILING DATE: 1999-04-05
; PRIOR PILING DATE: 1999-04-05
; PRIOR FILING DATE: 1999-04-10
; PRIOR FILING DATE: 1999-04-10
; PRIOR FILING DATE: 1999-01-13
; PRIOR PILING DATE: 1999-01-13
; PRIOR PILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR PILING DATE: 1999-01-13
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; PRIOR FILING DATE: 1998-06-15
; PRIOR FILING DATE: 1998-06-15
; PRIOR FILING DATE: 1998-04-03
; NUMBER CO SEQ ID NOS: 30
; SOFTWARE: FRANCENTE TOWN NUMBER: US 09/055,010
; SOFTWARE: FRANCENTE TOWN NUMBER: US 09/055,010
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 95.4%;
Matches 2550; Conservative
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CORGANISM: Homo sapiens
US-09-417-455-6
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GENERAL INCLEARTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
FILE REFERENCE: 28110/35801
CURRENT APPLICATION NUMBER: US/09/348,942
CURRENT APPLICATION NUMBER: PCT/US99/04291
EARLIER APPLICATION NUMBER: US 09/281,210
EARLIER FILING DATE: 1999-04-05
EARLIER PILING DATE: 1999-02-17
EARLIER FILING DATE: 1999-02-17
EARLIER FILING DATE: 1999-01-13
EARLIER FILING DATE: 1999-01-13
EARLIER FILING DATE: 1999-01-13
EARLIER FILING DATE: 1999-01-13
EARLIER FILING DATE: 1998-06-19
EARLIER FILING DATE: 1998-06-10
EARLIER FILING DATE: 1998-06-10
EARLIER FILING DATE: 1998-06-15
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                   ; Sequence 6, Application US/09348942; Patent No. 6337072; GENERAL INFORMATION:
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LENGTH: 2648
TYPE: DNA
ORGANISM: Homo sapiens
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                                                            AATCGAGCTCTGCTCTGGTTGGTTGTAGTGATCAGGAAACAGATCTCAGCAAAG 1558
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GENERAL INFORMATION:
APPLICANT: FOCA, JOHN
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APPLICANT: POCA, ADDI
ITILE OF INVENTION: A MOVEL INTERLEUKIN-I RECEPTOR ANTAGONIST AND USES THERE
FILE REFERENCE: 28110/36010
CURRENT APPLICATION NUMBER: US/09/457,626
CURRENT APPLICATION NUMBER: US 09/417,455
BARLIER PILING DATE: 1999-10-13
BARLIER PILING DATE: 1999-10-13
BARLIER PILING DATE: 1999-10-13
BARLIER PILING DATE: 1999-00-07
BARLIER PILING DATE: 1999-00-07
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Pred. No. 0;
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Best Local Similarity 99.4
Matches 2550; Conservative
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; ORGANISM: Homo sapiens
US-09-457-626-6
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FRICK APPLICATION NUMBER: US 09/23,552
PRIOR PILING DATE: 2000-05-3-10
PRIOR PELING DATE: 1999-12-08
PRIOR PELING DATE: 1999-12-08
PRIOR PELING DATE: 1999-12-08
PRIOR PELING DATE: 1999-10-13
PRIOR PELING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 09/149,45
PRIOR APPLICATION NUMBER: US 09/149,492
PRIOR PELING DATE: 1999-10-10-13
PRIOR PELING DATE: 1999-10-10-13
PRIOR PELING DATE: 1999-10-10-13
PRIOR PELING DATE: 1999-10-10-13
PRIOR APPLICATION NUMBER: US 09/25,30
PRIOR APPLICATION NUMBER: US 09/25,30
PRIOR APPLICATION NUMBER: US 09/25,30
PRIOR APPLICATION NUMBER: US 09/22,591
PRIOR APPLICATION NUMBER: US 09/22,591
PRIOR PELING DATE: 1999-0-1-3
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RESULT 5 US-09-576-008-6 Sequence 6, Application US/09576008 ; Patent No. 6541623

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                                                    GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMCRPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FEBLESEQ for Windows Version 4.0
SEQ ID NO 956
LEASTH 2720
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Pred. No. 0;
0; Mismatches 11; Indels
                           Sequence 956, Application US/09949016
Patent No. 6812339
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Best Local Similarity 99.4
Matches 2550; Conservative
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CRGANISM: Human
US-09-949-016-956
RESULT 6
US-09-949-016-956
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                                                                                                                                             3,
                                                                                                                    Length 9634;
                                                                                                                                            8; Indels
                                                                                                                    DB 4;
                                                                                                                 Score 2245.2;
Pred. No. 0;
0; Mismatches
                       4.0
        207012
Windows Version
                                                                                                                87.6%;
                                                                                                                             Best Local Similarity 99.5
Matches 2283; Conservative
       NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 12698
LENGTH: 9634
                                                          TYPE: DNA
CRGANISM: Human
US-09-949-016-12698
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Bacent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT FILING DATE:
CURRENT PAPLICATION NUMBER: US/09/949,016
FILE REFERENCE: C1001307
CURRENT FILING DATE: 2000-04-14
FRIOR FILING DATE: 2000-10-20
FRIOR PAPLICATION NUMBER: 60/231,768
FRIOR FILING DATE: 2000-10-09
FRIOR PAPLICATION NUMBER: 60/231,498
FRIOR FILING DATE: 2000-0-0-09
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Pred. No. 0;
0; Mismatches
CURRENT FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 09/348,942
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-04-05
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Best Local Similarity 99.1%;
Matches 2274; Conservative
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Pred. No. 0;
0; Mismatches
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 8 LENGTH: 7605
                                                                                                                                 86.6%;
99.1%;
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Matches 2274; Conservative
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CORGANISM: Homo sapiens
US-09-348-942-8
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TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES

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FILE REPERENCE: 28110/38101

CURRENT APPLICATION NUMBER: PCT/US99/04291

EARLIER APPLICATION NUMBER: PCT/US99/04291

EARLIER FILING DATE: 1999-04-05

EARLIER PLING DATE: 1999-04-05

EARLIER PLING DATE: 1999-02-17

EARLIER PLING DATE: 1999-02-17

EARLIER PLING DATE: 1999-02-17

EARLIER PLING DATE: 1999-01-13

EARLIER PLING DATE: 1998-07-31

EARLIER PLING DATE: 1998-06-19

EARLIER PLING DATE: 1998-06-15

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Patent No. 6337072
GENERAL INFORMATION:
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6004 CATGAAAAAGTGCTCATGACATATTGAGAAGACCTACTTACAAAGTGGCATATATTGCAA 6063 1230 TITATTTTAATTAAAAGATACCTATTTATATATTTTTATTAAAAAAAA	TAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGAGGCTGTGCTGAGTTTGTG TAGTGATCAGGAATCTCAGCAAAGCCACTGAGGAGGAGGAGGAGGAATTGTG TGGCTGGAATCTCTGGCTAAGGAACTTAAAGAACACAAAATCATCTGGTAATTCTTTCCTA TGGCTGGAATCTCTGGGTAAGGAACTTAAAGAACAAAAATCATCTGGTAATTCTTTCCTA TGGCTGGAATCTCTGGGATTCCAAGGACTTGGAAAATCATCTGGTAATTCTTTCCTA GAAGGATCACACCCCTGGGATTCCAAGGACTTGGATACTCTGGTAATTCTTTCCTA ACGGTTGAATTGTGTCCCCCTCCAAATTCACATCCTTCTGGAATCTCTGGTAATTCTTTCCTA ACGGTTGAATTGTGTCCCCCTCAAATTCACATCCTTCTTGGAATCTCTGGTAATTCTTTCGAACTTTTTTTT	2130 CAGCAGCTCTAGGAAACTAATACAGCTGCTAAAATGATCCCTGTCTCTCGTGTTTACAT 2189

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                                                                                                                                                                                                                                            APPLICATION: A NOVEL INTERLEUKIN-1 REGERENCE: 28110/36456
CURRENT APPLICATION NUMBER: US/09/576,008
CURRENT APPLICATION NUMBER: US/09/576,008
CURRENT FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: US 09/457,626
PRIOR PILING DATE: 1999-12-08
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-04-05
PRIOR PILING DATE: 1999-01-17
PRIOR PILING DATE: 1999-01-13
PRIOR PILING DATE: 1999-01-13
PRIOR PILING DATE: 1999-01-13
PRIOR PILING DATE: 1998-05-20
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                                                                                                                               Sequence 8, Application US/09576008
Patent No. 6541623
GENERAL INFORMATION:
2563
                      Query Match
Best Local Similarity 95.1%;
Matches 2274; Conservative
                                                                                                                                                                                             APPLICANT: Ford, John
APPLICANT: Ho, Alice Suk-Yue
TGCAGAGAAAGAGA
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SOFTWARE: FastSEQ for
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LENGTH: 7605
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FILE REPERENCE: 28110/36328

CURRENT APPLICATION NUMBER: US/09/417,455

CURRENT FILING DATE: 1999-10-13

PRIOR APPLICATION NUMBER: US/09/417,455

PRIOR FILING DATE: 1999-0-0-7

PRIOR FILING DATE: 1999-0-0-7

PRIOR FILING DATE: 1999-0-4-05

PRIOR FILING DATE: 1999-0-4-05

PRIOR FILING DATE: 1999-0-6-15

PRIOR FILING DATE: 1999-0-6-15

PRIOR FILING DATE: 1999-0-6-13

PRIOR FILING DATE: 1999-0-6-13

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Pred. No. 0;
5; Mismatches
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OTHER INFORMATION: n = A,T,C or
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98.9%;
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Best Local Similarity 98.9
Matches 1663; Conservative
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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RESULT 13
US-09-417-455-7
Sequence 7, Application US/09417455
Patent No. 6294655
GENERAL INPORMATION:
APPLICANT: Pord, John
APPLICANT: Pace, Ann

5510 1768 5570 1828 5630 1888 5690

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GENERAL INFORMATION:

APPLICANT: Ford, John
APPLICANT: Pace, Ann
APPLICANT: Pace, Ann
FILE PEREIGNEZ: 28110/3610
CURRENT APPLICATION NUMBER: US/09/457,626
CURRENT FILING DATE: 1999-12-08
ARLIER APPLICATION NUMBER: US 09/417,455
EARLIER FILING DATE: 1999-0-13
EARLIER FILING DATE: 1999-0-0-3
EARLIER FILING DATE: 1999-0-0-3
EARLIER FILING DATE: 1999-0-0-6
EARLIER FILING DATE: 1999-0-0-6
EARLIER FILING DATE: 1999-0-0-6
EARLIER FILING DATE: 1999-0-1-3
EARLIER FILING DATE: 1998-0-1-3
EARLIER FILING DATE: 1998-0
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Pred. No. 0;
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Patent No. 6426191
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### MATCHES 1663; CORRETABLIVE 5; Mismatches 9; Indels 4; Gaps 4; 4073 AGCAGTGAACACATGAGGCTCACCTTCT 310 4073 AGCAGTGAACACATGAGGCTCACCTTCTTGTTGCCACAGGAATCCAACAGCTTCACCTTCT 4132 4073 AGCAGTGAACACATGAGGCTTCACCTTCTTCTTTTTTTTT	CTGCCACTGTCATATGCTACCTTTCCTTTCTTCCTCATCATCTTGTTGTGGGGGGGG

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March 13, 2005, 10:45:20 ; Search time 22.9062 Seconds (without alignments) 10854.228 Million cell updates/sec Run on:

US-09-617-720A-3 Title: Perfect score:

Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 seqs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_16Dec04:* 1: qeneseqn1980s:* Database

geneseqn1980s:* geneseqn1990s:*

geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* geneseqn2002as:* geneseqn2002bs:* geneseqn2001as:* geneseqn2001bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:*

	Description	Aaf27923 Human IL-	Aaf27926 Interleuk	Aaf27950 Interleuk	_	Aaf31356 Extension	Abz77451 Extended	Aag95200 Simple ta	Continuation (7 of	Adj75968 Marker ge	Ads36459 Human aut	Adc24703 Human wil	Ada02876 Human DPT	Adb72614 Human DPT	Adc85355 Mouse Dpt	Adm74471 Human car	Adc87426 Human GPC	Abt10752 Human bre	Abl32170 Human imm	Abk88541 Human cho	Aaz98056 Human sec
SUMMARIES	ΩI	AAF27923	AAF27926	AAF27950	AAZ30053	AAF31356	ABZ77451	AAQ95200	ABD32923 6	ADJ75968	ADS36459	ADC24703	ADA02876	ADB72614	ADC85355	ADM74471	ADC87426	ABT10752	ABL32170	ABK88541	AAZ98056
	DB	2	S	'n	7	4	œ	7	13	12	13	10	σ	10	10	12	10	9	9	9	т
	Query Match Length DB	42	73	6540	7605	7605	7605	446	110000	4579	165156	335199	52661	52661	52661	52661	59588	74822	3973	496	867
٠	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	78.6	76.2	74.8	74.8	74.8	73.3	73.3	73.3	73.3	73.3	73.3	72.4	71.0	71.0
	Score	42	42	42	42	42	42	33	32	31.4	31.4	31.4	30.8	30.8	30.8	30.8	30.8	30.8	30.4	29.8	29.8
	Result No.	-	7	m	4	ß	9	7	&	o U	10	c 11	12	13	14	15	c 16	c 17	18	19	c 20

Aad11669 Human sec Abx69765 Human sec Acc50425 Human sec Abz71239 Human sec Adb21132 Human sec Adc73483 Human sec Adc73483 Human sec Adc3595 Human sec Adc35912 Human sec Acc50392 Human sec Adc35915 Gene enco Adf289151 Human Gal Acc4096 Human imm Acc143928 Mouse pro Ada0269 Mouse pro Ada0269 Mouse Pri Add372407 Mouse Pri Add372407 Mouse Pri Add372407 Mouse Pri Add372407 Mouse Pri Add369917 Mouse Pri Add3600 Mouse Pri Add	Agustigo numan cir
AAD11669 ABK69765 ACC50425 ACC50425 ABZ71239 AD871239 AABZ71239 AAA15236 AAA15236 AAA15236 AAA15236 AAA152915 AAAC50392 AAAC50392 AAAC50392 AAAC5006 AAAA1006 AAAA1006 AAAA1006 AAAA1006 AAAA4006 AAAA1006 AAAAA1006 AAAAA1006 AAAAA1006 AAAAAA1006 AAAAAAAAAA	2011
4 9 8 8 8 8 4 1 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0
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24 4 4 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1) F
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

ALIGNMENTS

Human IL-IL1 coding sequence 5' end #2. BP. AAF27923 standard; cDNA; 42 (first entry) 08-MAY-2001 AAF27923; RESULT 1 AAF27923

Human; IL-IL1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis; chromosone 2q13; inflammatory disease; heart disease; Graves' disease; rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer; osteoporosis; systemic luque erythematosus; ss.

sapiens. Homo WO200105974-A2.

25-JAN-2001.

17-JUL-2000; 2000WO-US019508.

99US-0144298P. 16-JUL-1999; (INTE-) INTERLEUKIN GENETICS INC.

Nicklin M, Barton J;

WPI; 2001-091974/10.

Nucleic acids encoding human and murine interleukin-1L1 polypeptides useful for controlling inflammatory processes.

Claim 21; Fig 1; 150pp; English.

The present invention provides the protein and coding sequences of the human and murine interleukin-ILI (IL-ILI) proteins. The IL-ILI gene is located between the IL-Ibeta and IL-Ireceptor genes at human chromosome 2q13. The sequences are useful in the diagnosis, prevention and treatment of heart disease, cancer and inflammatory diseases such as rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disorder, diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,

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BP.

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Human; IL-III; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis; chromosome 2q13; inflammatory disease; heart disease; Graves' disease; rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;
                                                                                                                              Interleukin-IL1 genomic sequence.
                 AAF27950 standard; DNA; 6540
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                    WO200105974-A2
                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUL-1999;
                                                                                                                                                                                                                                                             Unidentified.
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                                                                                           08-MAY-2001
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                                                      AAF27950;
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AAF27950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of heart disease, cancer and inflammatory diseases such as rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disorder, diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis, severe periodontal disease and pregnancy complications. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; IL-IL1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis; chromosome 2q13; inflammatory disease; heart disease; Graves' disease; rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;
severe periodontal disease and pregnancy complications. The present sequence is one of two alternative 5' ends of the human IL-IL1 coding
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human and murine interleukin-1L1 polypeptides useful for controlling inflammatory processes.
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                                                                                                              DB 5; Length 42;
                                                                                                                                                   0; Indels
                                                                                                                                                                                       1 AAGGAAGGAGGAAAGGAAGGAGTGAAGGAAGGAGTGAAA 42
                                                                                                                                                                                                                          1 AAGGAAGGAGAAAGGAAAGGAAGGAAGGAAGGAGTGAAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 73 BP; 31 A; 5 C; 33 G; 4 T; 0 U; 0 Other;
                                                                         Sequence 42 BP; 19 A; 0 C; 21 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                osteoporosis; systemic lupus erythematosus; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence is an IL-IL1 coding sequence fragment
                                                                                                                              0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Interleukin-IL1 coding sequence fragment #1.
                                                                                                                                                   0; Mismatches
                                                                                                              Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INTE-) INTERLEUKIN GENETICS INC.
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                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                     AAF27926 standard; DNA; 73
                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2001 (first entry)
                                                                                                                                                   42; Conservative
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Best Local Similarity
                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200105974-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JUL-1999;
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                                          sednence
                                                                                                                                                   Matches
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AAF27926
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The present invention provides the protein and coding sequences of the human and murine interleukin-ILI (IL-ILI) proteins. The IL-ILI gene is located between the IL-Ibeta and IL-Ireceptor genes at human chromosome 2q13. The sequences are useful in the diagnosis, prevention and treatment of heart disease, cancer and inflammatory diseases such as rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disorder, diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis, severe periodontal disease and pregnancy complications. The present sequence is the IL-ILI gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; interleukin-1 receptor; IL-1; antagonist; sepsis; acute pancreatitis; endotoxic shock; cytokine induced shock; rhemmatoid arthritis; chronic inflammatory arthritis; pancreatic cell damage; diabetes mellitus type 1; graft versus host disease; inflammatory bowel disease; inflammation; pulmonary disease; autoimmune disease; inflammatory disease; antiproliferative; myelogenous leukemia; premature labor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   murine interleukin-1L1 polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 6540;
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, 0.0015;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480 AAGGAAGGAGGAGAAGGAAGGAGTGAAGGAAGGAGTGAAA 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding a human interleukin-1 receptor antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAGGAAGGAGGAAAGGAAGGAAGGAAGGAAGGAGTGAAA 42
osteoporosis; systemic lupus erythematosus; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human and murine interuseful for controlling inflammatory processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Scc...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                         17-JUL-2000; 2000WO-US019508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity luv..
Best A2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                  Nicklin M, Barton J;
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Gaps

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42

RESULT 3

42; Conservative

Matches

ò 원 interleukin; IL-1 receptor; cancer; inflammation; ds.

Extension of genomic clone B2HFLS20W

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The present sequence encodes a human interleukin-1 (IL-1) receptor antagonist. It is an extension of AAZJ0052. The encoded polypeptide is capable of binding IL-1 receptors (IL-1Rs). The polymucleoides and polypeptides can be used for the prevention or treatment of disorders involving sepsis, acute pancreatitis, endotoxic shock, cytokine induced shock, rheumatorid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary call disease, other autoimmune disease or inflammatory disease, ann antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine artification of premature labor secondary to intrauterine activity, cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, hematopoiesis regulating activity, tissue growth activity, activity, hematopoiesis regulating chemokinetic activity, hemostatic and thrombolytic activity, receptor/chemokinetic activity, activity, the products can also be used for detection, diagnosis and drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated interleukin-1 receptor binding polypeptides, used to treat e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease, inflammatory disease, autoimmune disease or proliferative disease.
intrauterine infection; nutritional activity; hematopoiesis regulating activity; tissue growth activity; hematopoiesis regulating activity; chemotactic activity; chemotactic activity; chemotactic activity; anti-inflammatory activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7605 BP; 2081 A; 1647 C; 1865 G; 2007 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crkvenjakov R, Dickson M, Drmanac S, Labat I;
D, Kita D, Ford J, Pace A, Alfenito M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 42; DB 2; Length 7605; 100.0%; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 10A-C; 123pp; English
                                                                                                                                                                                                                                                                               98US-00055010.
98US-00079909.
98US-00099118.
98US-00127698.
99US-0025951.
                                                                                                                                                                                                                                            99WO-US004291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-611042/52
                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEO INC.
                                                                                                                                                                                                                                                                                                                         20-MAY-1998;
19-JUN-1998;
31-JUL-1998;
                                                                                                                                                               WO9951744-A2
                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-1999;
17-FEB-1999;
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Isolated nucleic acids encoding interleukin-1 (IL-1) receptor antagonist proteins (referred as IL-1Hy1), useful in the treatment of cancer, e.g. breast adenocarcinoma and brain tumors, and an inflammatory disease

WPI; 2001-071582/08.

13-OCT-1999; 99US-00417455. 08-DEC-1999; 99US-00457626. 10-MAR-2000; 2000US-0053552. 22-MAY-2000; 2000US-00576008.

(HYSE-) HYSEQ INC.

Ford J, Pace A;

07-JUL-2000; 2000WO-US018710

WO200102571-A2 Homo sapiens

11-JAN-2001

99US-00348942

07-JUL-1999;

Disclosure, Fig 10; 179pp; English.

mediated by IL-18

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The present invention relates to interleukin (IL)-1 receptor antagonist proteins. IL-IHy1 is useful for treating cancer, an inflammatory disease mediated by IL-18, inflammation resulting from infection or allergic reactions, and inflammation associated with chronic bronchitis, arthritis, diabetes or endothermia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Extended genomic DNA sequence of a human Interleukin-1Hy1 (IL-1Hy1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7605 BP; 2079 A; 1647 C; 1865 G; 2009 T; 0 U; 5 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 7605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 100.0%; Score 42; DB 4; Length 76 Local Similarity 100.0%; Pred. No. 0.0015; Local 42; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1339 AAGGAAGGAGAGAAGGAAGGAGTGAAGGAAGGAGTGAAA 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAGGAAGGAGGAGAAGGAAGGAGTGAAGGAAGGAGTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allergic rhinitis; IgA production; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUL-2001; 2001US-0307754P.
29-NOV-2001; 2001US-0334668P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JUL-2002; 2002WO-US023845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Matches
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Gaps

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0; Mismatches

42; Conservative

Matches

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Local Similarity

1 AAGGAAGGAGGGAAGGGAAGGAGGAAGGAGGAGTGAAA 42

1338

AAF31356 standard; DNA; 7605

05-APR-2001 (first entry)

AAF31356;

RESULT 5
AAP31356
ID AAP3
XX
AC AAF3
XX
XX
XX

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Identifying simple tandem repeat loci in DNA - by screening DNA library to enrich for fragments contg. the repeats before cloning and rescreening, also simple tandem repeats for treatment or diagnosis.
                                                                                                                                                                                                                                                                                                                                                     Armour J;
                                                                                                                                                                                                                                                                                                                                          (UYLE-) UNIV LEICESTER
                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-240682/31.
                         WPI; 2003-239438/23
    (HYSE-) HYSEQ INC
               Lin H,
                                                                                                                                                                                                                                                  08-FEB-1996
                                                                                                                                                                                                                                                                                                WO9517522-A2
                                                                                                                                                                                                                                                                                                                     21-DEC-1994;
                                                                                                                                                                                                                                                                                                                                21-DEC-1993;
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                                                                                                                                                                                                                                                                                                           29-JUN-1995
                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                        AAQ95200;
                                                                                                                                                                     Query Match
Best Local S
               Ho AS,
                                                                                                                                                                                Matches
                                                                                                                                                                                                                   RESULT 7
AAQ95200
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AAQ95200 is a simple tandem repeat (STR) corresponding to wg2b3. The STR can be used for treatment and diagnosis in human and veterinary medicine, partic. for genetic characterisation, mapping, linkage studies and analysis/diagnosis of acquired disease alleles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bronchial asthma; chronic obstructive pulmonary disease;
respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS ABD32923 Accession Abd32923
                                                                                                                                                                                   Score 33; DB 2; Length 446;
Pred. No. 0.63;
0; Mismatches 5; Indels
                                                                                                                                                   Sequence 446 BP; 164 A; 47 C; 190 G; 44 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AAGGAAGGAGGAGAAGGAAGGAGTGAAGGAAGGAGTGAA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAGGAAGGAGAAAGGAAAGGAGTGAAGGAAGGAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                  Continuation (7 of 8) of ABD32923 from base 600001 WP Sequence split into 8 fragments LOCUS ABD32923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 32; DB 1
; Pred. No. 1.9;
0; Mismatches
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710000
788759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; marker gene; gene; ds.
                  Claim 26; Page 25; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-2003; 2003EP-00254857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ75968 standard; DNA; 4579
                                                                                                                                                                                           78.6%;
87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.2%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500001
600001
700001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100001
                                                                                                                                                                                                                                                                                                                                                                                                                                               Begin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similaricy ches 35; Conservative
                                                                                                                                                                                           Query Match
Best Local Similarity 87.8
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Fragment Name
ABD32923_0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABD32923_1
ABD32923_2
ABD32923_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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ABD32923 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
ABD32923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                             The present sequence encodes human interleukin (IL)-IHy1 polypeptide. IL-
IHy1 inhibitors are used in the method of the invention. The
specification describes a method of inhibiting B-cell proliferation,
c specification or differentiation. The method comprises administering an
cutivation or differentiation. The method comprises administering an
inhibitor of IL-IHy1 activity to a human with elevated B-cell levels or
cactivity, in an amount that inhibits B-cell proliferation induced by IL-
IHy1. The method is useful for inhibiting or stimulating B-cell
proliferation, activation or differentiation in patients having a B-cell
related disorder (e.g. lymphoma, leukemia, myseloma or infection) or an
autoimmune disease (e.g. allergy, asthma or allergic rhinitis), or in
screening for compounds that modulate B-cell differentiation. The IL-IHY1
polypeptide, or the inhibitor of IL-IHy1 activity, is useful in preparing
differentiation or activation. The IL-IHy1 polypeptide may also be used
in preparing a medicament for reducing IgA production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simple tandem repeat; STR; wg2b3; treatment; genetic; diagnosis; characterisation; mapping; linkage studies; analysis; alleles; ss
                                                                                                                                  Inhibiting or stimulating B-cell proliferation, activation or differentiation, useful for treating B-cell-related disorders or autoimmune diseases, comprises administering an interleukin-1Hyl polypeptide or its inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7605 BP; 2079 A; 1647 C; 1865 G; 2009 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 100.0%; Score 42; DB 8; Length 7605; Local Similarity 100.0%; Pred. No. 0.0015; es 42; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1339 AAGGAAGGAGGAGAAGGGAAGGAGTGAAGGAAGGAGTGAAA 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simple tandem repeat (STR) corresponding to wg2b3
                                                                                                                                                                                                                                   Disclosure, Page 111-113; 115pp, English
                                                            Rupp F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ95200 standard; DNA; 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                            Ford JE,
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(Human cancer-associated genomic DNA F

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Gaps

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Gaps

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5; Indels

Length 110000;

Yamaya M, Kubo H, Nagai H, Izuhara K;

Ohtani N, Sugita Y, (GENO-) GENOX RES INC

WPI; 2004-193155/19.

06-AUG-2002; 2002JP-00229312. 20-MAR-2003; 2003JP-00077212.

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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial colls are stimmlated with interleukin-13, or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimmlated with interleukin-13. Also described: (1) a reagent (1) for certified with interleukin-13. Also described: (1) a reagent (1) for certified with interleukin-13 and described: (1) a reagent (1) for certified with interleukin-13 asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a hordinal asthma or chronic obstructive pulmonary disease; (5) a marker gene for bronchial asthma or chronic obstructive pulmonary disease; (5) a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polymuclecide that suppresses the carborial asthma or a chronic obstructive pulmonary disease, comprising to a protein encoded by a marker gene; and (7) a DNA chip for testing for expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a group and antiasthmatic activities, and can be used in gene therapy. The method con an immobilised to assay a marker gene (1) has respiratory
Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bronchial asthma or chronic obstructive pulmonary disease. The pr
sequence is used in the exemplification of the present invention.
                                                                                                                                                    Example 11; SEQ ID NO 1220; 241pp; English.
                                                                                                healthy subject
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Gaps Seguence 4579 BP; 1124 A; 1151 C; 1149 G; 1155 T; 0 U; 0 Other; 74.8%; Score 31.4; DB 12; Length 4579; 85.4%; Pred. No. 2.3; 6; Indels 0; 85.4%; 35; Conservative Best Local Similarity Query Match Matches

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2753 AAGGAAGGAGGAAGGAAGGAAGGAAGGAAGGAA 2713 1 AAGGAAGGAGGAAGGAAGGAGTGAAGGAAGGAGTGAA 41 ઠે g

ADS36459 standard; DNA; 165156 BP. ADS36459;

16-DEC-2004 (first entry)

Human autoimmune disease-related genomic DNA sequence - SEQ ID 1673

single nucleotide polymorphism detection; SNP detection; rheumatoid arthritis; type 1 diabetes; multiple sclerosis; systemic lupus erythematosus; inflammatory bowel disease; psoriasis; thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo; glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease; primary systemic vasculitis; ds.

Homo sapiens

WO2004083403-A2

30-SEP-2004.

18-MAR-2004; 2004WO-US008461

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genetic polymorphisms associated with an altered risk of developing an autoimmune disease (e.g. rheumatoid arthritis). The invention further comprises a method of identifying an individual that has an altered risk of developing an autoimmune disease, comprising detecting a single nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA and protein sequences of the invention are useful for diagnosing and treating autoimmune diseases, such as: rheumatoid arthritis, type 1 diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory bowel diseases, psoriasis, thyroiditis, celiac disease, pernicious anaemia, asthma, vitiligo, glomerulonephitis, Grave's disease, myocarditis, Sjogran's disease, or primary systemic vasculitis. The present nucleic acid represents a human autoimmune disease related genomic DNA sequence of the invention. NOTE: The present sequence is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         shown in the specification, but has been retrieved from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 165156 BP; 45717 A; 35582 C; 35601 G; 47895 T; 0 U; 361 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                               New isolated nucleic acid molecule comprises at least 8 contiguous muclochides Where one of the nucleotides is a single nucleotide polymorphism (SNP), useful for diagnosing or treating autoimmune diseases, e.g. rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises amino acid and coding sequences containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31.4; DB 13; Length 165156; Pred. No. 2.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                      Claim 16; SEQ ID NO 1673; 123pp; English.
                                                                                                                      Alexander HC;
18-MAR-2003; 2003US-0455444P.
25-APR-2003; 2003US-0465241P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.8%;
Best Local Similarity 85.4%;
Matches 35; Conservative
                                                                                                                    Cargill M, Begovich AB,
                                                                       (APPL-) APPLERA CORP.
                                                                                                                                                                   WPI; 2004-728480/71
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ADC24703 standard; DNA; 335199 BP 18-DEC-2003 (first entry) ADC24703; ADC24703/c

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ds, nootropic, neuroleptic; tranquillizer; gene therapy, synaptogenesis, mutation, neurological disease; mental disorder; psychiatric illness; autism; Asperger syndrome; schizophrenia; attention deficit hyperactivity disorder. Human wild type HNL4Y genomic sequence. Location/Qualifiers number= 1b 08500. .109001 10299. .108499 .0156. .10298 ๙ 'number= /*tag= Homo sapiens intron exon

/number= 2 109002. .205868 /*tag= d /number= 2

intron

tag= c

exon

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Gaps

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Indels 41

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Pred. No. 3.1; 0; Mismatches

74.8%; ilarity 85.4%; Conservative

1 AAGGAAGGAGGAGAAGGGAAGGAAGGAAGGAAGGAGTGAA

Score 31.4; DB 10; Length 335199; Pred. No. 3.1;

intron

exon

intron

intron

exon

intron

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exon

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mental disease. This sequence corresponds to the genomic sequence of the human wild type HNL4Y gene.
wild-type forms of the nucleic acid and polypeptide can be used similarly. Also detecting mutations in the nucleic acid and polypeptide, or measuring activity of the polypeptide, can be used to detect biochemical disorders that affect formation of synapses and to diagnose
                                                                                              Sequence 335199 BP; 98958 A; 63589 C; 65677 G; 106975 T; 0 U; 0 Other;
                                                                                                                                        Best Local Similarity
Matches 35; Conserv
                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated or purified polynucleotide encoding a polypeptide (the wild-type form of which is involved in synaptogenesis) that includes at least one mutation associated with development of neutological disease and/or a predisposition to development of mental disorders or psychiatric ilnness. The polypeptide are used to screen for agents that modulate their activity. Also nucleic acid, polypeptide, polypeptide-specific antibodies, vectors containing he nucleic acid and host cells containing the vector, are useful as pharmaceuticals for treating mental and neurological disorders, specifically autism, Asperger syndrome, schizophrenia and attention deficit hyperactivity disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid encoding mutant protein involved in synaptogenesis, tul for treatment and diagnosis of e.g. autism, Asperger syndrome, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leboyer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Betancur C,
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(ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; SEQ ID NO 4; 416pp; French.
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.310596
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                                                                                   .209679
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  .205928
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235028.
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310597.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bourgeron T,
Gillberg C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-2003
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acid sequences from mouse and human (ADAO1482-ADAO3094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using a random. Many of these do not carry transduced host oncogenes or at random with great genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carcinoma (especially breast cancer, prostate cancer, lymphoma or leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The present sequence represents a specifically claimed human CA mucleic acid sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to recombinant carcinoma associated (CA) nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
Human DPT carcinoma associated gene, SEQ ID NO:1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1394; 245pp; English
                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                  ADA02876 standard; DNA; 52661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-DEC-2002; 2002WO-US041414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-DEC-2001; 2001US-00035832.
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-587068/55.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; ds.
                                                                                                                                                                                                                                                                                                           ADA02876;
                                                                                                                                 RESULT 12
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carcinoma-associated gene; CA;

Cytostatic; gene therapy; vaccine; cancer; secreted; transmembrane; intracellular; ds.

02-DEC-2002; 2002WO-US038582,

WO2003045230-A2

Mus sp.

05-JUN-2003

30-NOV-2001; 2001US-00997722

(SAGR-) SAGRES DISCOVERY

Engelhard EK;

Morris DW,

WPI; 2003-513603/48.

ADC85355 standard; DNA; 52661 BP.

(first entry)

01-JAN-2004

ADC85355

Mouse Dpt coding sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                      Gaps
                                                                                                        Sequence 52661 BP; 15800 A; 11001 C; 11082 G; 14778 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 52661 BP; 15800 A; 11001 C; 11082 G; 14778 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                          Query Match 73.3%; Score 30.8; DB 9; Length 52661; Best Local Similarity 83.3%; Pred. No. 4.1; Matches 35; Conservative 0; Mismatches 7; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                  13858 AGGGAGGGAGGAAGGAAGGATTGAAGGAAGGAAA 13899
                                                                                                                                                                                                                                                                                                                   cancer; neoplasm; adenocarcinoma; sarcoma; gene.
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in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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83.3%; Pred. No. 4.
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23-CCT-2001, 2001US-00004113.
08-NOV-2001, 2001US-00052482.
30-NOV-2001, 2001US-00937722.
20-DEC-2001, 2001US-00034650.
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New recombinant nucleic acid comprising a nucleotide sequence of any of the carcinoma-associated (CA) genes, useful for screening for drug

candidates for diagnosing or treating carcinomas.

Claim 1; SEQ ID NO 141; 983pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, carcinoma associated nucleic acid, CA nucleic acid, gene, ds, carcinoma associated protein, CAP; carcinoma; leukaemia; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 52661 BP; 15800 A; 11000 C; 11083 G; 14778 T; 0 U; 0 Other;
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Pred. No. 4.1;
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83.3%;
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Best Local Similarity 83.3
Matches 35; Conservative
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13858 AGGAGGAGGAAGGAAGGATTGAAGGAAGGAAG 13899

RESULT 14 ADC85355

1 AAGGAAGGAGGAAAGGAAGGAGTGAAGGAAGGAGTGAAA 42

DB 10; Length 52661;

22-DEC-2000; 2000US-00747377. 02-MAR-2001; 2001US-00798586.

(MORR/) MORRIS D W. (ENGE/) ENGELHARD E K.

Engelhard EK Morris DW,

WPI; 2004-328562/30

New carcinoma associated gene or protein, useful for preparing a composition for diagnosing or treating carcinoma e.g., leukemia or lymphoma.

Claim 1; SEQ ID NO 142; 29pp; English

The invention relates to new recombinant nucleic acids. The invention also relates to a host cell comprising a recombinant nucleic acid or expression vector, an expression vector comprising a recombinant nucleic acid, a recombinant protein, a method of screening for drug candidates, a method of screening for a bioactive agent capable of binding to a carcinoma associated protein (QAP) encoded by a nucleotide sequence, a carcinoma drug, a method of evaluating the effect of a candidate carcinoma drug, a method of diagnosing carcinoma, a method for inhibiting carcinoma drug, a carcinoma. A method of evaluating the effect of a candidate carcinoma drug comprises administering the diagnosing carcinoma or propensity to carcinoma. A method of evaluating the effect of a candidate carcinoma drug comprises administering the drug to a patient, removing a carcinoma drug comprises administering the full of a candidate carcinoma drug comprises administering the full of a patient of a gene comprising the nucleotide sequence. A method of diagnosing carcinoma comprises determining alterations in the carcinoma activation of a gene comprising the nucleotide sequence. A method of diagnosing carcinoma comprises determining the expression of the gene comprising the nucleic acid sequence in a first tissue type from the first individual and comparing the expression of the gene from a second normal tissue type from the first individual and comparing the carcinoma. A method of inhibiting the carcinoma comprises administering to a patient of the CAP. Treating carcining a patient an inhibitor to the CAP. Treating carcining a patient and nucleic and agent sneedific.

Carcinomas comprises administering to a patient an inhibitor to CAP. Preating carcinoma comprises administering to a patient an inhibitor of CAP. Apprentice of the patient Neutralising the effect of a CAP comprises contacting an agent specific for the CAP. The polypeptide specifically binds to the protein encoded by the nucleic acid. It comprises an antibody that specifically binds to the protein encoded by the nucleic acid. The nucleic acid are useful for preparing a composition for diagnosing or treating carcinoma e.g., leukaemia or lymphoma. This sequence represents a human carcinoma associated (CA) nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 52661 BP; 15800 A; 11001 C; 11082 G; 14778 T; 0 U; 0 Other;

Gaps 73.3%; Score 30.8; DB 12; Length 52661; 83.3%; Pred. No. 4.1; tive 0; Mismatches 7; Indels 0; 35; Conservative Query Match Best Local Similarity Matches 35; Conserva

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1 AAGGAAGGAAGAAAGGGAAGGAAGGAAGGAAGGAAGTGAAA 42

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Search completed: March 13, 2005, 12:34:23 Job time: 29.5729 secs

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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The il-11 gene and polypeptide products
Patent: WO 0105974-A 1 25-JAN-2001;
Interleukin Genetics, Inc. (US)
Location/Qualifiers
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Submitted (09-JUN-1999) Nicklin M.J., Division of Molecular and
Genetic Medicine, University of Sheffield, Royal Hallamshire
Hospital, Glossop Road, Sheffield, S10 2JF, UNITED KINGDOM
Location/Qualifiers
                                                          AAGCAGAGACTCTGTGAGATAATCGATGTTTGTTTTTAAGTTGCTCAGTTTTGGTCTA
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'note="between IL1B and IL1RN"
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| Organism="Homo sapiens"
| Mol_type="mRNA"
| db xref="taxon:9606"
| Chromosome="2"
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Homo sapiens (human)
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Mammalia; Eutheria; Primates;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (09-JUN-1999) Nicklin M.J., Division of Molecular a
Genetic Medicine, University of Sheffield, Royal Hallamshire
Hospital, Glossop Road, Sheffield, S10 2JF, UNITED KINGDOM
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                                              GAACAAAATCATCTGGTAATTCTTTCCTAGAAGATCACAGCCCCTGGGATTCCAAGGC 1679
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AY359117 2598 bp mRNA linear PRI 03-OCT-2003 HOMO Sapiens clone DNA96787 IL1HY1 (UNQ1896) mRNA, complete cds. AY359117 AY359117.1 GI:37183350

RESULT 7
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VPNRWLDAZLSPVILGVQGGSQCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYR
RDWGLTSSFESAAYPGWFLCTVPEADQPVRLTQLPENGGWNAPITDFYFQQCD"
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Homō sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (01-MG-2001) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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98.1%; Score 2514.2;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2552; Conservative 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DNA9678"
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		2077 TCTGCTGAACCTTAATCTCCAGCCTCCTGAACGAAGAATAATTTCGG 2136 2100 CTGTTTTAAGCCACCAGAGTTACAGCCTCCTGAACGAAGAATAAATTTCGG 2136 2100 CTGTTTTAAGCCACCAGGATAATTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCT 2159 2137 CTGTTTTAAGCCACCAGGATAATTGGTTACAGCTCTAGGAACTAATACAGCTGCT 2196 2150 AAAATGCTCCCTGTCTTTTAGATTACATTCTGTGTGTCCCCTCCCACAATGTACCA 2219 2197 AAAATGATCCTCTCTCTGTTTTTAATTCTGTGTGTGTCCCCTCCCACAATGTACCA 2256 2220 AAGTTGTCTTTGTGACCCAATAGAATATGGCAGAAGTGGTGCCCCTCCAAATGTACCA 2239 2257 AAGTTGTCTTTGTGA-CCAATAGAATATGGCAGAAGTGGATGCACTTCCAAGATT 2315 2257 AAGTTGTCTTTGTGA-CCAATAGAATATGGCAGAAGTGATGCCACTTCCAAGATT 2315	2280 AGGTTATAAAAGACACTGCAGCTTCTACTTGAGCCCCTCTCTCT
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Butfard, G.G., Blakesley, R.W., Touchman, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
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                             BCO24747

Homo sapiens interleukin 1 family, member 5 (delta), transcript

Variant 2, mRNA (cDNA clone MGC:29840 IMAGE:4996939), complete cds.
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Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowig, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2692)
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Submitted (01-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiML)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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KEYWORDS
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REFERENCE
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TITLE
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                                                                                                                  ACCESSION
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COMMENT
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RESULT 8
BC024747
LOCUS
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/translation="WYLSGALCFRWKDSALKV1YLHNNQLLAGGLHAGKVIKGEEISV
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                                                                                                              / Dote= synonyms: FIL1(DELTA), FIL1D, IL1RF3, IL1HY1, FIL1, IL1LA, MGC29840"

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98.0%; Score 2512; D
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2551; Conservative 0; Mismatches
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AY-1998 US 09/127698,13-JAN-1999 US 09/229591 PR
BD-1999 US 09/221370
JOHN PORD, ANN PACE
CIENTS/09, A61K38/00, C07K14/52, C07K14/545, C07K16/24, C12N1/15,
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CTCTGCTGAAACC1TAATCTCAGACTTCCAGCCTCCTGAACGAAGAAGAATAAATTTCG
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                    GCTGTTTTAAGCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAAACTAATACAGCTGC
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                                                                                                                        CCAATCTATCTTGGCTCACTCGCTCTGGGGAAGCTAGCTGCCATGCTATGAGCAGGCCT
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1 (bases 1 to 2648)
1 ford, J. and Pace, A.
Interleukin-1 receptor antagonist and
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Location/Qualifiers
1. 2648
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/mol_type="unassigned DNA"
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Sequence 6 from patent US 6337072.
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1352 GIGGCAGTATAGGGGATTTTTCTTTTAATTCTGTTAATTTATCTGTATTTCCTAATTTT 1411
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TGGCCCAGCCCCACCCCTTCCCTTTAATCCTGCCACTGTCATATGCTACCTTTCCTATC 105:
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Unclassified. REFERENCE 1 (bases 1 to 2648) AUTHORS Ford,J., Ho,A.S.Y. and Pace,A. TITLE Interleukin1 receptor antagonist and uses thereof JOURNAL Patent: US 654162-A 6 0.1-APR-2003; FEATURES 1. Location/Qualifiers Source 1.2648 Acganism="unknown" /mol_type="genomic DNA"	Query Match 97.1%; Score 2488.4; DB 6; Length 2648; Best Local Similarity 99.4%; Pred. No. 0; Matches 2550; Conservative 0; Mismatches 11; Indels 5; Gaps 5;	Oy 1 AGGGAGTCTACACCCTGTGGAGCTCAAGATGGTCCTGAGTGGGCGCTGTGCTTCCGAA 60	QY 61 TGAAGGACTCGGCATTGAAGGGCTTTATCTGCATAATAACCAGCTTCTAGCTGGAGGGC 120	OY 121 TGCATGCAGGAAGGTCATTAAAGGTGAAGAGATCAGCGTGGTCCCCAATCGGTGGCTGG 180	Oy 181 AIGCCAGCCTGTCCCCGTCATCCTGGGTGTCCAGGGTGGAAGCCAGTGCCTGTCATGTG 240	Oy 241 GGGTGGGGCAGCGCCTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 300	0y 301 GTGCCAAGAATCCAAGAGCTTCACCGTCTACCGGGGGACATGGGGGTCACCTCCAGCT 360	Oy 361 TCGAGTCGGCTGCCTACCCGGGTTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCTG 420	QY 421 TCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACT 480 L	QY 481 TCCAGCAGTGTGACTAGGGCAACGTGCCCCCCAGAACTCCCTGGGCAGAGCCAGGTCGG 540 L	Oy 541 GTGAGGGGTGAGGAGACCCATGGGGGACAATCACTTTCTGCTCTCAGGACCCC 600	Oy 601 CAGGICTGACTTAGTGGGCACCTGACCACTTTGTCTTCTGGTTCCCAGTTTGCATAAATT 660	Oy 661 CTGAGATTTGGAGCTCAGGCTCCTCCCCCACTGGATGGTGCTACTGCTGTGGAAC 720	Oy 721 CTTGTAAAAACCATGTGGGGTAAACTGGGGAATAACATGAAAAAGATTTCTGTGGGGGTGGG 780	Oy 781 GIGGGGGAGTGCTGGGAATCATTCCTGCTTAATGGTAACTGACAAGTGTTACCCTGAGCC 840	Oy 841 CCGCAGGCCAACCCAGTTGAGCCTTATAGGGTCAGTACCACATGAAGTC 900
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1999) Functional Genomics, HYSEQ Inc., 670 yvale, CA 94086, USA Qualifiers	Qy qq	721 CTTGTAAAAACCATGTGGGGTAAACTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGG 780
1. 2720 Organism="Homo sapiens" Mol_type="mRNA" db_xref="taxon:9606"	ζς qa	781 GTGGGGGGTGTGGGGAATCATTCCTGCTTAATGGTAACTGACAGAGTGTTACCCTGAGCC 840
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ore 2488.4; DB 9; Length 2720;	yy du	1020 TCTTCCCTCATCATCTTGTTGTGGGCATGAGGAGGTGGTGATGTGTCAAAGAAATGGTTCG 1079 1153 TCTTCCCTCATCATGTTGTGGGGATGAGGAGGTGGTGATGTGTGAGAAAGAAAGAAATGGCTCG 1212
OBSERVATIVE 0; MISMACCHES 11; INGELS 5; GADS 5; AGGGGAGTCTACACCCCTGTGGAGCTCAAGATGGTCCTGAGTGGGGCGCTGTCCTTCCGAA 60	کې م <u>و</u>	1080 AGCTCAGAAGATAAAAGATAAGGGTATGCTGATCCTCTTTTAAAAACCCAAGATACA 1139

Qy 2219 AAAGTTGTCTTTGTGA-CCP Db 2353 AAAGTTGTCTTTGTGA-CCP Qy 2279 TAGGTTATAAAAGACACTGC Qy 2339 CCAATCTATCTTGCACTGCTATT Qy 2339 CCAATCTATCTTGGCTCACT Qy 2339 ATAAAGAGACTTACGTGGTR Qy 2339 ATAAAGAGACTTACGTGGTR Qy 2459 AGAAGCAGAGACTTACGTGGTR Qy 2532 ATAAAGAGACTTACGTGGGTR Db 2592 AGAAGCAGAGACTTACGTGGGTR Qy 2592 AGAAGCAGAGACTTTACGTGGCAAT Db 2592 AGAACTTGTTATGCAGCAAT Db 2552 CTAACTTGTTATGCAGCAAT	arch complet i 113	
ATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAGTGCTCATGACATATTGAGAA 119 ATCAAAATCCCAGATGTTGTTTTTTCCTATTCCCATGAAAAGTGCTCATGACATATTGAGAA 133 GACCTACTTACAAAGTGCGCATATA-TTGCAATTTATTTAATTAAAAGATACCTATTTT 125 GACCTACTTACAAAGTGGCATATATTTGCAATTAATTTAAATAAA	AGAGCAGAATCATCTCTGATTGTCCTCAGCCTCCCCTGAGTAAATTGAATTGTGATGTGAGCAGAATCCCCCCAGAATTGTTGTGATTGTTGATTCCCCCCCTGAGAACAGTTCAGCAAGGGAACACAAGGGAACTTAA 151 CCACTGAGGAGGCTCTGGTTGGTTGGTTGGATGAACAATCTCTGGGAACTTAA 151 CCACTGAGGAGGAGGCTGTTGTTGGTTGGATGAACAATCTCTGGGTAAGGAACTTAA 175 CCACTGAGGAGGAGGCTGTTGTTGGTTGGATGAACAATCTCTGGGTAAGGAACTTAA 175 CCACTGAGGAGGAGGCTGTTGTTTGGTTGGTTGAATCTCTGGGAATCTCTGGGATTCCAAGG 181 CCACTGAGAGAGGCTGTTGTTTGGTTGGTTGAATCTTTGGGAATCTCTGGGATTCCAAGG 181 CCACTGAGAGAGGCTGTTGTTTTCTTTCTTTCTTAAAAAATCCATCGAATTTCTTTTCTAAAAAAATCATCAAAAAAATCATCTGGTAATTCTTTTCTTTTTTTT	2233 GCTGTTTTAAGCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAAACTAATACAGCTGC 2292 2159 TAAAATGATCCCTGTCTCCCTGTGTTTACATTCTGTGTGTCCCCTCCCCACAATGTACC 2218 2293 TAAAATGATCCCTGTCTCCTCGTGTTTACATTCTGTGTGTCCCCTCCCCACAATGTACC 2352
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GGAGCTTCTACTTGAGCCCTCTCTCTGCCACCCACGGCC 2338 PATAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGAT 2278 CTCGCTCTGGGGGAAGCTAGCTGCCATGCTATGAGCAGGCCT 2398 TAAAAAATGAAGTCTCCTGCCCACAGCCACATTAGTGAACCT 2458 AGATAATCGATGTTTGTTGTTTT-AAGTTGCTCAGTTTTGGT 2517

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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The il-111 gene and polypeptide products
The il-111 gene and polypeptide products
Patent: WO 0105974-A 3 25-JAN-2001;
Interleukin Genetics, Inc. (US)
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AR221131

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Homo sapiens mRNA for interleukin-1-like protein 1 (ILIL1 gene)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (09-JUN-1999) Nicklin M.J., Division of Molecular a
Genetic Medicine, University of Sheffield, Royal Hallamshire
Hospital, Glossop Road, Sheffield, S10 2JF, UNITED KINGDOM
Location/Qualifiers
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                 Nicklin,M. and Barton,J.
The il-111 gene and polypeptide products
Patent: WO 0105974-A 16 25-JAN-2001;
Interleukin Genetics, Inc. (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol type="mRNA"
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/chromosome="2"
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Nicklin, M.J.
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HSA242738
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I. (bases 1 to 2692)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausberg, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Alschul, S.F., Zeeberg, B., Buetow, K.H., Scheder, C.F., Bhat, N. K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Haich, F., Diatchenko, L., Marusina, K.D., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Rah, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Hale, S., Garciach, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schnutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                      BC024747 linear PRI 30-JUN-2004 HOMO sapiens interleukin 1 family, member 5 (delta), transcript variant 2, mRNA (cDNA clone MGC:29840 IMAGE:4996939), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 42 Row: k Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27894309. Location/Qualifiers
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Web site: http://www.hgsc.bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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Submitted (01-MRZ-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                   Gaps
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Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
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0
                               Length 2604;
Score 42; DB 9; Lengtn 20. Pred. No. 0.0014;
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Contact: MGC help desk
       100.0%; Scc. 100.0%; Pred. No. v. 0; Mismatches
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Query Match
Best Local Similarity 100...
These 42; Conservative
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                                                                                                                                                                                                                   Barton, J.L., Herbst, R., Bosisio, D., Higgins, L. and Nicklin, M.J. A tissue specific IL-1 receptor antagonist homolog from the IL-1 aluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities Eur. J. Immunol. 30 (11), 3299-3308 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (17-3NN-2000) Nicklin M.J.H., Division of Molecular and
Genetic Medicine, University of Sheffield, Royal Hallamshire
Hospital, Sheffield, South Yorkshire, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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gene="ILILI"
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4234. .6522)
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IL1L1 gene; interleukin-1 like protein 1.
Homo sapiens (human)
Homo sapiens
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/note="alternative"
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/gene="IL1L1"
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/gene="IL1L1"
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/gene="IL1L1"
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/gene="IL1L1"
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/gene="IL1L1"
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Nicklin, M.J.H.
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  4J271338
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                                                                                                                                                                                                                                                                          /noce="symonyms: FIL1(DELTA), FIL1D, IL1RP3, IL1HY1, FIL1, IL1L1, MG229840"

MD_xxef="LocusID:26525"

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens ILLL1 gene for interleukin-1 like protein 1, exons
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                                                                                                            /tissue type="Placenta, choriocarcinoma"
/clone_lib="NIH_MGC_10"
/lab_host="DH10B"
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| mol_trype="mRN"s" |
| db xref="taxon:966"
| clone="MGC:29840 IMAGE:4996939"
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The il-111 gene and polypeptide products
Patent: WO 0105974-A 43 25-JAN-2001;
Interleukin Genetics, Inc. (US)
Location/Qualifiers
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                                                                                                                                                                                                 'note="Vector: pCMV-SPORT6"
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/db_xref="taxon:9606"
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Sequence 43 from Patent WO0105974.
AX080431
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                                                                                                                                                                                                                                                      gene="IL1F5"
                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="IL1F5"
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/product="interleukin-1 receptor antagonist homolog 1"
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RDMGLTSSFESAAYPGWFLCTVPEADQPVRLTQLPENGGWNAPITDFYFQQCD"
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PN JP 2002510492-A/6

PD 09-APR-2002

PF 03-APR-1999 US 09/055010,15-MAY-1998 US 09/079909 PR 03-APR-1998 US 09/08264,19-JUN-1998 US 09/1229591 PR 17-PEB-1999 US 09/127698,13-JAN-1999 US 09/229591 PR DOIN PORD, ANN PACE PC CI2N15/09,A61K38/00,C07K14/52,C07K14/545,C07K16/24,C12N1/15,PC C12N1/19.

PC C12N1/19.

PC C12N1/19.

PC C12N1/21,C12N5/10,C12Q1/68,G01N33/50,G01N33/56,G01N33/56,PC
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source 1. .7605
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oin(2088. .2116,3504. .3589,4777. .4904,5106. .5330)
/gene="ILLHY1"
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100.0%; Pred. No. 0.0011;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.0011;
iive 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
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JP 2002510492-A/6.
Homo sapiens (human)
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gene, complete cds.
AF216693.1 GI:8572054
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2 (bases 1 to 7604)
2 (bases 1 to 7604)
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1 (bases 1 to 7604)

Mulero,J.J., Nelken,S.T. and Ford,J.E.
Organization of the human interleukin-1 receptor antagonist gene ILHYI
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/join(1857) .1890,2061. .2116,3504. .3589,4777. .4904,
5106. .7394)
/gene="ILHYI"
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5106. .7394)
/gene="ILIHY1"
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1306. 7394
/gene="ILiHY1"
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                                                                                                                                                                                                                                                                                                                             4033. .4233
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4234. .6522
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/number=6
                                                                                        2631. .2716
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           1249. .2630
/gene="IL1L1"
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Homo sapiens
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ACO16724 197308 bp DNA linear PRI 09-JAN-2002
Homo sapiens BAC clone RP11-339F22 from 2, complete sequence.
AC016724
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The sequence of Homo sapiens BAC clone RP11-139F22
The sequence of Homo sapiens BAC clone RP11-139F22
J (bases 1 to 197308)
Waterston, K.H.
Buinted (04-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Meterston, University School of Medicine, 4444 Forest Park Parkway, No. Louis, Waterston, R.H.
                                                                                                                                                                                                                                           PAT 25-JAN-2001
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Sulston, J.E. and Waterston, R. Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                   Length 7605;
                                                                                                                                                                                                                                                                                                                                                                                                                                A interleukin-1 receptor antagonist and uses thereof
Patent: WO 0102571-A 8 11-JAN-2001;
HYSEQ, INC. (US)
                                                   Query Match 100.0%; Score 42; DB 6; Length 76 Best Local Similarity 100.0%; Pred. No. 0.0011; Matches 42; Conservative 0; Mismatches 0; Indels
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                           AX069311 7605 bp
Sequence 8 from Patent W00102571.
   /mol_type≂"genomic DNA"
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                                                                                                     Unclassified.
1 (bases 1 to 7605)
Pord, J. and Pace,A.
Interleukin-1 receptor antagonist and recombinant production
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For (Jasse 1 to 7605)

For (Jasse 1 to 7605)

Interleukin--1 receptor antagonist and uses thereof patent: US 6541623-A 8 01-APR-2003;

Locaticn/Qualifiers
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Ford, J. and Pace, A.
Assays involving an IL-1 receptor antagonist
Patent: 18 6426191-A 8 30-JUL-2002;
Location/Qualifiers
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Location/Qualifiers
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Sequence 8 from patent US 6426191.
AR221131
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Sequence 8 from patent US 6541623.
AR302959
Sequence 8 from patent US 6337072.
AR181997
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                                   AR181997.1 GI:20224913
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note="similar to Homo sapiens EST AA587127 (NID:92397941)
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/note="similar to Homo sapiens EST A1034379 (NID:g3255332)
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'note="similar to Homo sapiens BST BI091273
(NID:914509603)"
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4822 .4957
/rpt_family="MER1_type"
5152 .5337
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/rpt family="MER1_type"

8344. 9429

/rpt family="L2"

/rpt family="ERV1"

/rpt family="ERV1"

8999. .9029

/rpt family="CRV1"
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/rpt_family="MER1_type"
13540. 13855
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6118. .7901
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4311. .4450
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:1587. .11611
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1651. 11884
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1838_ .1952
/rpt_family="ERV1"
2105_ .2161
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/rpt_family="L2"
8008. .8145
/rpt_family="L2"
8146. .8347
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.2198. .12353
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18067. .18089
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2245. .2587
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12578. .12714
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9167. 9564
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10187. 10267
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/rpt_family="L1"
3460. .3481
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1074. .11122
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7526. .17822
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  917. .1361
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1362. .1814
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3235. .4195
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(http://bacpgc.med.buffalo.edu)
  Submitted (14-JUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
MO 63108, USA
Stasses I to 197308)
St. Louis, Materston, R.
Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington Submitted (09-JAN-2002)
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jul 14, 2001 this sequence version replaced gi:13431151.
Center: Washington University Genome Sequencing Center
Center code: WGSCC
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NEIGHBORING SEQUENCE INFORMATION:
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-725J3; the clone sequenced
to the right is RP11-97J14. Actual start of this clone is at base
position 1 of RP11-319F22; actual end is at base position 197308 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Data from AC084280 and AC024704 was used to finish this clone, AC016724. Polymorphisms have been identified between AC024704 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                             NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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Location/Qualifiers
                                                                                                                                                                                                                                                                         Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
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/db_xref="taxon:9606"
/chromosome="2"
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5. .275
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/rpt_family="L1"
744. .907
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Direct Submission
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FEATURES

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MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
MoPherson, Department of Genetics, Washington University, St. Louis
MCPherson, Department of Genetics, Washington University, St. Louis
MMO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
  Submitted (03-APR-2003) Genome Sequencing Center, Washington Induversity School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 162771)
                                                                                                                                                                                                                                                                                                                                                                                      NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEIGHBORING SEQUENCE INFORMATION:
This sequence is not the entire insert of the clone. This clone is
overlapped by AC108073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8 The Clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
Washington
                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
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                                                                                                                                                                                                                                                                                Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H_NH0366H04
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/rpt_family="BRVL"
1557. 1850
/rpt_family="Alu"
2004. 2097
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/rpt_family="MaLR"
2808. . 2905
/rpt_family="MaLR"
2906. . 3219
/rpt_family="Alu"
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Submitted (17-MAR-2003) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Bases 1 to 16271)
Sulston,J.E. and Wilson,R.
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Homo sapiens BAC clone RP11-366H4 from 4, complete sequence.
ACI38781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 42; DB 9; Length 197308; Best Local Similarity 100.0%; Pred. No. 0.00066; Matches 42; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt family="ERVL"
27616. .28020
/note="match to EST AW937349 (NID:98112771)"
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Haglund, K. and Kim, K.
The sequence of Homo sapiens BAC clone RP11-366H4
Upublished (2001)
3 (bases 1 to 162771)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
/rpt_family="MER1_type"
19604. .20083
                                                                                                                                                                                                                                                            /rpt_family="ERVL"
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22668. .22977
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                                                                                                                                                    21033. .21306
/rpt_family="L1"
21315. .21656
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Waterston, R.H.
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5 (bases 1 to 162771)
Waterston, R.H.
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28743.
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15248. .15536

/rpt_family="Alu"

15545. .15890

/rpt_family="L1"

15877. .15896

/rpt_family="MER2_type"

15977. .16280

/rpt_family="MeR2_type"

15977. .16280
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/rpt_family="(TA)n"
14507. .14574
/rpt_family="Alu"
14582. .14896
/rpt_family="Alu"
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4999. .5020
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5113. .5402
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                                                                                                                           family="Alu" .4583
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Homo sapiens BAC clone RP11-458M1 from 4, complete sequence.
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Submitted (03-DEC-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
S (Dases 1 to 179257)
Waterston, R. H.
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Submitted (29-JAN-2003) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179257)
2018ton, J. B. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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S Wang, C., Cotton, M., Meyer, R., Haakenson, W. and Bielicki, L.
The sequence of Homo sapiens BAC clone RP11-458M1
L Unpublished (2001)
B 3 (bases 1 to 179257)
S Waterston, R.H.
Direct Submission
L Submitted (13-SEP-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Parkway, St. Loud (6108), USA
E 4 (bases 1 to 179257)
S Waterston, R.H.
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Submitted (07-FEB-2003) Department of Genetics, Washington
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6 (bases 1 to 179257)
Waterston, R.
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jan 29, 2003 this sequence version replaced gi:26006685.
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Center code: WUGSC Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu

Center project name: H_NH0458M01

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions. This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong wectors: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION: This sequence is the entire insert of the clone. Location/Qualifiers

FEATURES

1. .179257

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Query Match 82.4%; Score 34.6; DB 9; Length 179257; Best Local Similarity 90.2%; Pred. No. 0.17; Matches 37; Conservative 0; Mismatches 4; Indels 0;
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Maximum I
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04-SEP-2003
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                                                                                                                                                                                                                                                                                                                                    Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (European Molecular Blology Laboratories,
Heidelberg/Germanny) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 338)
Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Miemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST (Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., et al.)
Unpublished (2003)
Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No si sequence available.

This clone (DKFZp68602193) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualiflers
                                                                                                                   DKFZp686022193_r1 686 (synonym: hlcc3) Homo sapiens CDNA clone DKFZp686022193_5', mRNA sequence.
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67;
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ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon.9606"
/clone="URYZp68602193"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .338
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                    Chordata; (Primates; (
                                                                                                                                                                                                                                 BX477358.1 GI:31674556
                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
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Mammalia; Eutheria;
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Gaps

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GSS 03-OCT-2000

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RESULT 3 CB745486/c

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LOCUS DEFINITION

ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

RESULT 2 AW141829/c LOCUS

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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

AUTHORS

REFERENCE

JOURNAL

COMMENT

TITLE

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AZ401556 100 264 bp DNA linear GSS 03-OCT-200 1M0168P17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0168P17 F, genomic survey sequence.
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:10116"
/clone="mrbe3-00043-a6"
/tissue_type="bxain B15"
/clone_lib="rat brain E15 (10374)"
/note="vector: pBCB; Site_1: BstXI; Site_2: Not1; rat brain B15"
             Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00043 row: a column: 6.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              64.1%; Score 25; DB 6; Length 444; 84.8%; Pred. No. 1.6e+02; ive 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: o168 row: P column: 17
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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                                                                                                                                                                        organism="Rattus norvegicus"
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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0168P17"
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Location/Qualifiers
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Mus musculus
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Matches 28; Conservative
Unpublished (2003)
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Fax: 801 585 7177
                                                                                                                                                 1. .444
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84112, USA
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JOURNAL
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AZ401556
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                  COMMENT
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EST291936 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone RGICI87 5' end similar to guanine nucleotide-binding protein Rar,
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                                                                                                                                                                                                                                                                                                                                                           Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMGNNUC: WRBE3-00043-A6-A rat brain E15 (10374) Rattus norvegicus CD745486 CD745486.1 GI:29812788
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 424)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-9208
Email: nhlee@tigr.org
For clone availability, additional sequence and expression
information related to this EST please check the TIGR Rat Gene
information related to this EST please check the TIGR Rat Gene
contact the ATCC (http://www.atcc.org/atcc.html). To order a clone
Seq primer: M13 Reverses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="embryo 8, 12, 18 dpc"
/clone_lib="Normalized rat embryo, Bento Soares"
/note="Vector: pT7T3Pac; Site_l: EcoRI; Site_2: NotI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:10118"
/clone="RGICI87"
                       14 AGACTCCACAGCTCCCGCCAGGAGAA 39
                                                           1 AGACTCCACACTCCCGCCAGGAGAA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
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Amgen EST Program.
Amgen Rat EST Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.8
Matches 28; Conservative
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AW141829
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FEATURES

ORIGIN

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Gaps

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BU354596 805 bp mRNA linear EST 28-NOV-2002
603473139F1 CSEQCHN70 Gallus gallus cDNA clone ChEST352n10 5', mRNA
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Gallus gallus
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 805)
Boardman, P.E., Samz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken CDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
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                                                          Length 854;
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Best Local Similarity 84.4%; Pred. No. 3.8e+02;
Matches 27; Conservative 0; Mismatches 5;
                                                   Score 24.8; DB 7;
Pred. No. 1.9e+02;
0; Mismatches 7;
                                                                                                                                                  3 GAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGA 38
                                                                                                                                                                                              57 gaggaccagacagaarceccagcrecerecaggga 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="ChEST352n10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TTGAGGAACAGGCAGACTCCACAGCTCCCGCC 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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BU354596.1 GI:25862597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simon Hubbard
                                                        63.6%;
80.6%;
                                                     Query Match
Best Local Similarity 80.6
Matches 29; Conservative
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BU354596/c
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PUBMED
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KEYWORDS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gql 47321141gbl AF125072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:30035315"
/lab host="DH10B TonA"
/clone=lib="NIH-MGC_256"
/note="Organ: oocyte; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; cDNA was primed using oligo-dT primer:
5'-pGACTAGATCAGAGGGGGGGCGCCC(T) 25-3' and cloned into
the EcoRV/Not1 sites of pExpress-1. Size-selection >0.5 kb
resulted in an average insert size of 1.2 kb. This is a
primarylibrary (normalized primary library is NIH-MGC 257)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH-MGC library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Daniels S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Betheads, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Kathleen Horner, Stanford University
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: NDAMIN89 row: d column: 12
High quality sequence stop: 562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Makaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 854)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT 30259104 NIH MGC_256 Mus musculus cDNA clone
IMAGE:30935315 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                63.6%; Score 24.8; DB 8; Length 264; 80.6%; Pred. No. 1.8e+02; ive 0; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 GAGGACCAGACAGAATCGCCAGCTCCCTCCAGGGGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GAGGAACAGGCAGA.CTCCACAGCTCCCGCCAGGAGA 38
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CO805958.1 GI:51020184
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Best Local Similarity
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CO805958/c
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ORGANISM

AUTHORS TITLE

REFERENCE

MEDLINE PUBMED

COMMENT

JOURNAL

DEFINITION

RESULT 7 BE993964

ACCESSION VERSION KEYWORDS SOURCE

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/tissue_transper="Epithelial, Muscle"
/dev stage="Lactating, Neonatal"
/lab_host="DH10B TonA"
/lab_host="DH10B TonA"
/clone_lib="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSport6.1; Site_1:
Not!: Site_2: EcoR!; Normalized cow cDNA intestinal
library in pCMVSport6.1, constructed from equinolar mRNA
pools derived from 5 sources, 4 lactating intestinal,
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal lleum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"
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1 (bases 1 to 523)
Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H. and Sugimoto,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alt '' -trim fasta. Vector identified -minmatch 12 -minscore 18
                                                                                                                                                                                         1 (bases 1 to 633)
Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
Matukumalli,L.K.
                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.0%; Score 23.8; DB 7; Length 633; 80.0%; Pred. No. 4.4e+02; ive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
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                                                                                                                                                                                                                                                                                                                                                                                          Bovine Functional Genomics Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="8BOV_22G04"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                  Contact: Richard G. Baumann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="Holstein"
                          GI:45056900
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AV604210
AV604210.1 GI:9734583
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Best Local Similarity 80.0°
Matches 28; Conservative
                                                                             Bos taurus (cow)
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                          CK831100.1
                                                                                                        Bos taurus
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/db_xref="taxon:10090"
/clone="ul-M=B21-bj-b-01-0-Ul"
/dev grage="27-32 days"
/lab_host="DB108 [Life Technologies)"
/lab_host="mul-mal BMAP MHI2 S1"
/clone lib="WHH BMAP MHI2 S1"
/note="vector: pj773D-pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; The NH BMAP MHI2 S1 library is a subtracted library derived from nouse hippocampus tissue. For a detailed description of the library from which this clone was derived, the library from which this clone was derived, the library from which this clone was derived, please
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence contained an oligo-dT track that was present in the coligonucleotide that was used to prime the synthesis of first coligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: 1-30, AT_rich#Low_complexity
                                                           BE993964
UI-M-BZ1-bjj-b-01-01.81 NIH BMAP MHIZ S1 Mus musculus cDNA clone UI-M-BZ1-bjj-b-01-0-UI 3', mRNA sequence.
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Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
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4054658 BARC 8BOV Bos taurus CDNA clone 8BOV_22G04 5', mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
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TAG_SEQ=None found"
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Pred. No. 4.3e+02;
7; Indels
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    .381
    /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                       musculus (house mouse)
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80.0%;
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Fax: 301 443 9890
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Tel: 301-838-0200
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqresfégenoscope.cns.fr, Web : www.genoscope.cns.fr, Web : wew.genoscope.cns.fr, Web : use grand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX373721

BX373721 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI071YH11 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria, Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1046)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDBr, Libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Bos taurus kidney fetus"
/note="Vector: pZL1; Site_l: Sal1; Site_2: Not1; Poly A
was deleted from a Not1 sīte"
Betablishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0BAK063CB10NM1&c=1718.f. Location/Qualifiers
                                                                                                                           Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                         Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
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| Da_xref="taxon: 5606"
| Clon="CSODIO1YH11"
| tissue_type="PLACENTA COT 25-NORMALIZED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             466 rcaedarcceacadacrccagrecrccaeccaecaeca 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23.6; DB 1;
Pred. No. 5.2e+02;
                                                                Nucleic Acids Res. 29 (22), E108 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="ElKI021D06"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="kidney"
/dev_stage="fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BX373721.1 GI:30438340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29; Conservative
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Best Local Similarity
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DEFINITION
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CE222012
tigr-gss-dog-17000333348863 Dog Library Canis familiaris genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP700567 Gada Taira anterior neuroectoderm (ANE) pCS105 cDNA library Xenopus laevis cDNA clone XL490c66ex 5', mRNA sequence. BP700567
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                                                                                                                                                                                                                                           Gaps
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Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K. Kusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9615"
/clone_lib="bog_Library"
/note="Site_l: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
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                                                                                                                                                                                    Length 1046;
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                                                                                                                                                                                                                                                                                                                           576 TCAAGAGCAAGGAGACTCAACTGCTCTCGCCAGTAGAA 613
                                                                                                                                                                                                                                                                                               2 TGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA 39
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                                                                                                                                                                                  Score 23.6; DB 5;
Pred. No. 5.3e+02;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Canis familiaris"
/mol_type="genomic DNA"
/strāin="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (dog)
Canis familiaris
                                                                                                                                                                                    Query Match
Best Local Similarity 76.3%;
Matches 29; Conservative
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BZ206975
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BZ206975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Trissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                 1 (bases 1 to 766)
Osada,S., Kitayama,A., Ueno,N. and Taira,M.
Expression analysis of genes which are expressed in the anterior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 794)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                 neuroectoderm of Xenopus embryos
Unpublished (2004)
Contact: Masanori Taira
Department of Biological Sciences
Graduate School of Science, University of Tokyo; CREST, Japan
Science and Technology Corporation, Japan
7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="anterior neuroectoderm" | dev stage="late gastrula (stage 12.5)" | /clone llb="Goada Taira anterior neuroectoderm (ANE) pCS105 cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.5%; Score 23.2; DB 5; Length 766; ilarity 77.8%; Pred. No. 7.4e+02; Conservative 0; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                  Tel: 81-03-5841-4434
Fax: 81-03-5841-4434
Email: m taira@biol.s.u-tokyo.ac.jp,
URL:http://www.shigen.nig.ac.jp/nbrp/xenopus/est/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Xenopus laevis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL490c06ex"
                                                               Xenopodinae; Xenopus; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: pYX-5
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Best Local Similarity
Matches 28; Conserv
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VERSION
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AUTHORS
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Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Email: Schao@tigr.org
Enail: Schao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
avalability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from Bac Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 425 row: O column: 8
Seg primer: 8P6
Class: BAC ends.
/clone="IMAGE:6415785"
/tissue_type="whole brain"
/dev stage="embryo 12.5 dpc"
/lab_host="DH10B (TI phage resistant)"
/clone lib="NIH BMAP FC0"
/clone lib="NiH BcoR I primer containing a Not I site. Double stranded containing a Not I site and then cloned directionally into pYx-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGAGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Amatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutues of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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CH230-42508.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-42508, genomic survey sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Shady, Shetty, L. Shatsman, S., Tsegaye, G., Geer, K.,
Shayartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Riggs, F. and Sequences from Library CHORI-230 Mbol segment
Unpublished (1999)
Other_GSS8: CH230-42508.TV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 59.5%; Score 23.2; DB 5; Best Local Similarity 75.7%; Pred. No. 7.4e+02; Matches 28; Conservative 0; Mismatches 9;
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|strain="BN/SsNHsd/MW"
|db_xref="taxon:10116"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 490)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

L Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: Capabb-rremail: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1107 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 477.
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wh83e11.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2387372 3',
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CHOR1-230 Rat (BN/SBNH8d/MCW) BĀC library produced by Pieter de Jong"
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 59.0%; Score 23; DB 8; 18est Local Similarity 74.4%; Pred. No. 8.4e+02; Matches 29; Conservative 0; Mismatches 10
/clone="CH230-42508"
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AI762761
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AI762761/c
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Gaps

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Query Match 58.5%; Score 22.8; DB 1; Length 490; Best Local Similarity 79.4%; Pred. No. 1e+03; Matches 27; Conservative 0; Mismatches 7; Indels

3 GAGGAACAGGCAGACTCCACAGCTCCCGCCAGGA 36

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278 GAGCAACAGGAAATTCCACAGCTGCCTCCAGAA 245
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Search completed: March 13, 2005, 18:13:56 Job time : 142.576 secs

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us-09-617-720a-2.rge

OM nucleic

Run on:

Sequence:

Searched:

Database

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HSA242737 2613 bp mRNA linear PRI 18-APR-2002
Homo sapiens mRNA for interleukin-1-like protein-1 (ILIL1 gene),
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                                              ALGOGOTI MOUSE DNA
AL359914 Human DNA
AC024443 Homo sapi
AC07950 Homo sapi
AC118274 Homo sapi
AC118275 Homo sapi
AC118275 Homo sapi
AC103106 Xenopus 1
AC14478 Pan trogl
BS000632 Pan trogl
BS000632 Pan trogl
BS000632 Pan trogl
AC102558 Mus muscu
AC102558 Rattus no
AC12742 Rattus no
AC12742 Rattus no
AC132742 Rattus no
AC132763 Rattus no
AC132860 Drosophil
AC13681 Drosophil
AC13680 Drosophil
  Homo sapi
Rattus no
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Human DNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 0.00058;
ive 0; Mismatches 0;
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AJ2427171 GI:6165333
ILLL1 gene; interleukin-1-like protein-1.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The il-ill gene and polypeptide products Patent: WO 0105974-A 2 25-JAN-2001; Interleukin Genetics, Inc. (US) Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .39
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                                                                                                                                                                                                                                                                                                                                                                                          AX080390 39 bp
Sequence 2 from Patent WO0105974.
AX080390 GI:13159841
                        AC127185
AF233337
AL606971
AL359914
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AC131689
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AC146478
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Best Local Similarity 100.0
Matches 39; Conservative
75.4 197308
65.1 90147
64.1 77303
63.6 91841
62.6 125499
61.0 177435
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59.5 198155
59.0 217447
59.0 214497
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59.0 214497
59.1 24588
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59.2 144096
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HSA242737
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   ORIGIN
                                                                                 March 13, 2005, 11:14:57 ; Search time 172.432 Seconds
  (without alignments)
  10959.418 Million cell updates/sec
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AZ282737 H
AZ28016 S
AF186094 H
BD211436 A
AR281130 S
AR281130 S
AR302958 S
AR3069310 S
AZ069310 S
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AX069311 8
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
                                                           nucleic search, using sw model
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AX080431
HSA271338
AF216693
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HSA242737
AX080406
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AF186094
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AR181996
AR221130
AR302958
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AR181997
AR221131
AR302959
AX069311
AC016724
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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39
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Perfect score:
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Regult Š .; 0

Gaps

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Indels

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54;

Length

DB 6;

PAT 03-FEB-2004

linear

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AF186094 2720 bp mRNA linear PRI 16-OCT-1999
Homo sapiens interleukin-1 receptor antagonist homolog (IL1HX1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryorda, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 2720)
Mulero, J. J., Pace, A. M., Nelken, S.T., Loeb, D.B., Correa, T.R., Drmanac, R. and Ford, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Direct Submission
Submitted (13-SEP-1999) Functional Genomics, HYSEQ Inc., 670
Almanor Ave., Sunnyvale, CA 94086, USA
1. .2720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lilhyl: A novel interleukin-1 receptor antagonist gene Blochem. Blophys. Res. Commun. 263 (3), 702-706 (1999) 99443727
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                                                      Score 37.4; DB 6. Pred. No. 0.0022; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent: WO 02068579-A 8735 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37.4; DB 6
Pred. No. 0.0011;
                                                                                                                                                                                                                                                                       CQ722801 2701 bp DNA Sequence 8735 from Patent WO02068579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 95.9%; Score 37.4; D
Best Local Similarity 97.4%; Pred. No. 0.00
Matches 38; Conservative 0; Mismatches

    2701
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  /db xref="taxon:9606"
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CQ722801.1 GI:42283658
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AF186094
AF186094.1 GI:6049804
                                                      Query Match
Best Local Similarity 97.4%;
Matches 38; Conservative
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Homo sapiens
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AUTHORS
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/protein_id="CAB59822.1"
/brotein_id="CAB59822.1"
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/db_xxef="COA,QUBH0"
/db_xxef="COA,QUBH0"
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RDMGLTSSFESAAYFGWFLCTVPEADQPVRLTQLPENGGWNAPITDFYFQQCD"
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                                                Barton,J.L., Herbst,R., Bosisio,D., Higgins,L. and Nicklin,M.J.
A tissue specific IL-1 receptor antagonist homolog from the IL-1
cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities
Eur. J. Immunol. 30 (11), 3299-3308 (2000)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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The il-111 gene and polypeptide products
Patent: WO 0105974-A 18 25-JAN-2001;
Interleukin Genetics, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="placenta"
/note="between IL1B and IL1RN"
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codon_start=1
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    .54
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"

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Sequence 18 from Patent WO0105974.
AX080406
                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ILILI"
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/evidence=experimental
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                                                                                                                                                                                                                                                                                                                                                                                                             /map="2q12-13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="IL1L1"
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Nicklin, M.J.
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Ford,J. and Pace,A.
Interleukin-1 receptor antagonist and recombinant production
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Ford, J. and Pace, A.
Assays involving an IL-1 receptor antagonist
Patent: US 6426191-A 7 30-JUL-2002;
Location/Qualifiers
1. .5751
/mol_type="genomic DNA"
     813 TGGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA 851
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Pred. No. 0.00092;
0; Mismatches 1;
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Location/Qualifiers
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AR221130
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AR302958
                                                                              Sequence 7 from patent US 6337072.
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/organism="unknown"
                                                                                                                                  AR181996.1 GI:20224912
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Best Local Similarity 97.4%;
Matches 38; Conservative
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Unclassified.
1 (bases 1 to 5751)
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                                                                                                              /note="IL-1ra homolog"
/codon grart=1
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/protein_id="AAP02757.1"
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RDMGLTSSFESAAXPGWFLCTVPEADQPVRLTQLPENGGWNAPITDFYFQQCD"
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CIZN1/21,C12N5/10,C12Q1/68,G01N33/50,G01N33/566,G01N33/68, PC
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1 (bases 1 to 5751)
Ford,J. and Pace,A.
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CI2N15/09, A61K38/00, C07K14/52, C07K14/545, C07K16/24, C12N1/15,
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09/099818 PR
09/229591 PR
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Patent: JP 2002510492-A 5 09-APR-2002;
HYSEQ INC
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95.9%; Score 37.4; DB 6;
Best Local Similarity 97.4%; Pred. No. 0.00092;
Matches 38; Conservative 0; Mismatches 1;
/organism="Homo sapiens"
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1. _2720

    .5751
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PR 03-APR-1998 US 09/05501

20-MAY-1998 US 09/082364,19-

31-UUL-1998 US 09/127698,13-

17-FEB-1999 US 09/251370
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JP 2002510492-A/5.
Homo sapiens (human)
Homo sapiens
                                                                  gene="IL1HY1"
                                                                                   163. .630
/gene="IL1HY1"
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09-APR-2002
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HSA271338 6540 bp DNA linear PRI 18-APR-2002
Homo sapiens ILIL1 gene for interleukin-1 like protein 1, exons
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Submitted (17-JAN-2000) Nicklin M.J.H., Division of Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Sheffield, South Yorkshire, UNITED KINGDOM Location/Qualifiers
1..6540
                                                                                                                                                                                                                                                                                                                                                                                                           Barton,J.L., Herbst,R., Bosisio,D., Higgins,L. and Nicklin,M.J.
A tissue specific IL-1 receptor antagonist homolog from the IL-1
cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities
Eur. J. Immunol. 30 (11), 3299-3308 (2000)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                        Gaps
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4234. .6522)
/gene="<u>i</u>lili"
ch 95.9%; Score 37.4; DB 6; Length 6540; 1 Similarity 97.4%; Pred. No. 0.0009; 18; Conservative 0; Mismatches 1; Indels 0
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                                                                           1 TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA 39
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AJ271338.1 GI:6729586
AJLL1 gene; interleukin-1 like protein 1.
Homo sapiens (human)
Homo sapiens
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Nicklin, M.J.H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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 Ford,J., Ho,A.S.Y. and Pace,A.
Interleukin--1 receptor antagonist and uses thereof
Patent: US 6541623-A 7 01-APR-2003;
Location/Qualifiers
1. .5751
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95.9%; Score 37.4; DB 6;
Best Local Similarity 97.4%; Pred. No. 0.00092;
Matches 38; Conservative 0; Mismatches 1;
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The il-111 gene and polypeptide products
Patent: WO 0105974-A 43 25-JAN-2001,
Interleukin Genetics, Inc. (US)
Location/Qualifiers
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Sequence 43 from Patent W00105974.
AX080431
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Sequence 7 from Patent W00102571.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /ous by DNA linear PAT 17-JUL-2003
A novel interleukin-1 receptor antagonist and uses thereof.
BD211437
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PN JP 2002510492-A/6

PD 09-APR-2002

PP 03-APR-1999 JP 2000542457

PR 03-APR-1999 US 09/055010,15-MAY-1998 US 09/079909 PR
20-MAY-1998 US 09/12568,13-JAN-1999 US 09/229591 PR
21-JUL-1998 US 09/12768,13-JAN-1999 US 09/229591 PR
21-JUL-1999 US 09/223170

PI JOHN PORD, ANN PACE

PC C12N15/09,461K38/00,C07K14/52,C07K14/545,C07K16/24,C12N1/15,PC C12N1/13,PC C12N1/11,C12N1/13,PC C12N1/13,PC C12N1/11,C12N1/13,PC C12N1/13,PC C12N1/11,C12N1/13,PC C12N1/11,C12N1/13,PC C12N1/11,C12N1/13,PC C12N1/11,C12N1/13,PC C12N1/11,C12N1/13,PC C12N1/11,C12N1/13,PC C12N1/13/PC C12N1/13/PC C12N1/13/PC C12N1/11,C12N1/11,C12N1/14,PC C12N1/113/PC C12N1/113/PC C12N1/113/PC C12N1/113/PC C12N1/11,C12N1/14,PC C12N1/14,PC C12N1/14,P
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1 (bases 1 to 7605)
1 (bases 1 to 7605)
2 Pord,J. and Pace,A.
A novel interleukin-1 receptor antagonist and uses thereof Patent: JP 2002510492-A 6 09-APR-2002;
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Homo sapiens
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RDMGLTSSFESAAYFGWFLCTVPEADQPVRLTQLPENGGWNAPITDFYFQQCD"
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Mulero,J.J., Nelken,S.T. and Ford,J.E.
Direct Submission
Submitted (15-DEC-1999) Functional Genomics, HYSEQ Inc, 670 Almanor
Ave., Sunnyvale, CA 94086, USA
Location/Qualifiers
1. .7664
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Mulero, J.J., Nelken, S.T. and Ford, J.E.
Organization of the human interleukin-1 receptor antagonist gene
                        . .1248,2631. .2716,3905. .4032,4234. .4458)
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                                                                                  function="putative cytokine or cytokine antagonist"
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VERSION
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AUTHORS
TITLE
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JOURNAL
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                                                                                                           Gaps
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Unclassified.
1 (bases 1 to 7605)
1 (bases 1 to 7605)
1 (bases 1 to 7605)
1 Interleukin-1 receptor antagonist and recombinant production thereof
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Query Match 95.9%; Score 37.4; DB 6; Length 7605; Best Local Similarity 97.4%; Pred. No. 0.00087; Matches 38; Conservative 0; Mismatches 1; Indels 0.
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Location/Qualifiers
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AR181997 7605 bp
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AR181997.1 GI:20224913
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AR181997
LOCUS
DEFINITION
ACCESSION
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AUTHORS
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Search completed: March 13, 2005, 15:49:14 Job time : 176.432 secs

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March 13, 2005, 10:45:20 ; Search time 1397.82 Seconds (without alignments) 10854.228 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Perfect score:
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RESULT 1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	921 Human IL-	:133 Human PRO	453 Human cDN	1229 Human PRO	Human	239 Novel hum	Human	438 Novel hum	1885 cDNA enco	061 cDNA enco	325 cDNA enco	224 Human sec	772 Human cDN	346 cDNA enco	319 Novel hum	Novel	Novel	1001 Novel hum	1523 Human PRO	448 cDNA enco
IES	Descr	Aaf2792:	Aaf92133	Abs7445;	Ab188229	Ab195718	Aca91239	Acd81616	Aca60438	Aca58885	Aca64061	Aca91325	Acd45224	Aca93772	Aca67346	Ach66319	. Acd02373	Aca89364	Aca69001	Aca98523	Aca63448
SUMMARIES	DB ID	5 AAF27921	4 AAF92133	6 ABS74453	6 ABL88229	6 ABL95718	8 ACA91239	8 ACD81616	8 ACA60438	8 ACA58885	8 ACA64061	8 ACA91325	8 ACD45224	8 ACA93772	8 ACA67346	8 ACH66319	8 ACD02373	8 ACA89364	8 ACA69001	8 ACA98523	9 ACA63448
	Length	2562	2598	2598	2598	2598	2598	2598	2596	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598
	& Query Match	100.0	98.1	98.1	98.1	98.1	98.1	98.1	98.1	98.1	98.1	98.1	98.1	98.1	98.1	98.1	98.1	98.1	98.1	98.1	98.1
	Score	2562	2514.2	2514.2	2514.2	2514.2	2514.2	2514.2	2514.2	2514.2	2514.2	2514.2	2514.2	2514.2	2514.2	2514.2	2514.2	2514.2	2514.2	2514.2	2514.2
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Adb17208 Human cDN	Ach03651 Human sec	Ada20013 Novel hum	Adb17396 Human cDN	Ada20185 Novel hum	Acd82165 Human sec	Ada00482 Human sec	Adb85724 Novel hum	Adb68403 Human PRO	Adb68210 Human PRO	Adb91027 Novel hum	Adc07107 Human PRO	Adc17286 cDNA segu	4 Novel	Adc52479 Novel hum	Add10604 Human sec	Add11564 Human sec	Add37357 Human sec	Add36155 Novel hum	Adg01156 Novel hum	Adg08709 Novel hum	Adf95330 Novel hum	Adh24183 Novel hum	Adh34209 Novel hum	Adh30042 Novel hum	10	
ADB17208	ACH03651	ADA20013	ADB17396	ADA20185	ACD82165	ADA00482	ADB85724	ADB68403	ADB68210	ADB91027	ADC07107	ADC17286	ADC14984	ADC52479	ADD10604	ADD11564	ADD37357	ADD36155	ADG01156	ADG08709	ADF95330	ADH24183	ADH34209	ADH30042	ALIGNMENTS	
o	σ	σ	σ	6	6	σ	6	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	9	10		
2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598	2598		
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2514.2	2514.2	514.	<u>.</u>	514.	2514.2	Ψ.	514.	2514.2	514.			514.	2514.2	Ψ.			2514.2	2514.2	514.	2514.2	2514.2	٠.	2514.2	14.		
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45		

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Human; IL-IL1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis; chromosome 2q13; inflammatory disease; heart disease; Graves' disease; rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer; osteoporosis; systemic lupus erythematosus; ss.
                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding human and murine interleukin-111 polypeptides useful for controlling inflammatory processes.
                                                                                                                                                                                              /*tag= a
/product= """IL-IL1""
/note= "this region is specifically claimed"
                                                                                                                                                                         Location/Qualifiers 30. .497
                                                                                                                                                                                                                                                                                                                                (INTE-) INTERLEUKIN GENETICS INC.
           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Fig 1; 150pp; English
           AAF27921 standard; cDNA; 2562
                                                                        Human IL-IL1 coding sequence.
                                                                                                                                                                                                                                                                                   17-JUL-2000; 2000WO-US019508.
                                                                                                                                                                                                                                                                                                          99US-0144298P.
                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                     Nicklin M, Barton J;
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                                                                                                                                                                                                                                          WO200105974-A2
                                                                                                                                                     Homo sapiens.
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                                                    08-MAY-2001
                                                                                                                                                                                                                                                               25-JAN-2001
                                AAF27921;
                                                                                                                                                                          Key
AAF27921
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The present invention provides the protein and coding sequences of the

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TIGGAICCAGICTCTAAGAAGGCIGCTGTACTGTTGTGTCCCCCCCCAAATTCAC 1740
 CCGCAGGCCAACCCATCCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTC 900
                                                                                                                                                                                                  1081 GCTCAGAAGATAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCCAAGATACAA
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                                             CTCTCACTCACCACTGTGCAGAGAGAGGGGGTGGTCATAGAGTCAGGGATCTATGGCCCT
                                                                                                   CTTCCCTCATCATCTTGTTGTGGGCATGAGGAGGTGGTGATGTCAGAAGAAATGGTTCGA
                                                                                                                                                                                                                 GCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAAGATACAA
                                                                                                                                                                                                                                                          TCAAAATCCCAGATGCTGCTCTCTATTCCCATGAAAAAGTGCTCATGACATATTGAGAAG
                                                                                                                                                                                                                                                                           TCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGCTCATGACATATTGAGAAG
                                                                                                                                                                                                                                                                                                                 AGCAGACATCATCTCTGATTGTCCTCAGCCTCCAATTCCCCAGAGTAAATTGAA
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human and murine interleukin-IL1 (IL-IL1) proteins. The IL-IL1 gene is located between the IL-lbeta and IL-Irceptor genes at human chromosome 2q13. The sequences are useful in the diagnosis, prevention and treatment of heart disease, cancer and inflammatory diseases such as rheumatoid arthitis, systemic lupus erythematosus, inflammatory bowel disorder, severe periodontal disease and pregnancy complications. The present sequence is the human IL-IL1 coding sequence
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Wood WI;
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                                                                                                                                                    Gerritsen ME,
Watanabe CK,
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30-MAR-2000; 2000WO-US008439.
25-APR-2000; 2000US-0199397P.
22-MAY-2000; 2000WO-US014042.
05-JUN-2000; 2000US-0209832P.
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1, Gurney AL,
                                                                                                       (GETH ) GENENTECH INC
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P-PSDB; AAB87601.
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99US-016495P.
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GUGGGGGGGGGGGGGGGGGGGGGGGAATCACTCTGGTTCCCTGTTCTGGTTCCCATTTGGATAATT 6 CACGTCTGACTTTGGGGCACCTGACCATTTGTTCTTCTGGTTCCCATTTGGATAATT 6 CACGTCTGACTTTGGACCTCACCACTTTGTTCTTCTGGATTCCCTGTTGGATAATT 6 CACGTCTGACTTTGGACCTCACCACTTTGTTCTTCTGGATTGCTTCTGTGAAAATT 6 CACGTCTGACATTTGGACCTCACCACTTTGTTCTTCTGGATTGCTTGTGAAAATT 6 CTGACATTTGGACCTCACTCACGACTCACCACTGAAAAATTGTTGTTCTGTGGAAAATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	

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antiarthritic, osteopathic, sports-related joint problem; articular cartilage defect, osteoarthritis, rheumatoid arthritis.
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98US - 0091628P
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98US - 00966757P
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01-SEP-1998;
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25-JUN-1998;
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The invention relates to an isolated secreted and transmembrane PRO polyeptide having 80 % sequence identity to a sequence ageneric ages of the protein and the peptide.

CC ARG5581-ARG55934 or their associated signal peptide are associated signal peptide are associated signal peptide are associated signal peptide and its associated signal peptide. Also included are the nucleic acids encoding the proteins with their associated signal peptide and associated signal peptide as the proteins are antibodies which specifically bind to the proteins. The proteins are subsected of containing and A. B. C or D polypeptide. By c or D in a sample with a polypeptide designated as B. C or D in 10 tolypeptide and determining the presence of an A. B. C or D polypeptide in the sample, where he formation of a A/E. B/F. B/G. C/H or D/I polypeptide and determining the presence of an A. B. C or D polypeptide in the sample, where he is a PRO1950 polypeptide. B is a PRO1950 polypeptide or a PRO1950 polypeptide and I is a PRO1950 polypeptide. F is a PRO1950 polypeptide. F is a PRO1950 polypeptide. F is a PRO1950 polypeptide. The sample comprises a call suspected of expressing the A. B. C or D polypeptide to a support. The proteins are useful for linking a bioactive molecule causes death of the cell as the E. F. G. H or I polypeptide apport: The bioactive molecule causes death of the cell. A. B. C or D or E. F. G. H or I The bioactive molecule causes death of the cell. A. B. C or D or E. F. G. H or I The bioactive molecule is a toxin, a radiolabel or an arbibode; and a polypeptide designated as A. B. C or D or E. F. G. F. G. H or I The bioactive molecule is a propertion of the proteins are useful for activity of a cell expressing a polypeptide designated as A. B. C or D or E. F. G. F. G. H. Or I The bioactive molecule is a polypeptide designated as A. B. C or D or E. F. G. F. G. H. Or I The bioactive molecule is a polypeptide designated as A. B. C or D or E. F. G. F. Or D or E. F. G. H. Or I The bioactive molecule are development and arti
                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis.
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Wood WI;
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Watanabe CK,
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2001WO-US017443.
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Grimaldi JC, Gurney
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P-PSDB; ABG95926.
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23-AUG-2000; 2
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20-DEC-2000; 2
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Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;

Pace S14.2; DB 6; Length 2558; Beet Load Siniarity 99.6; Pred. 90.0; Matches 2552; Conservative 0, Mismatches 8; Indels 3; Matches 2552; Conservative 0, Mismatches 8; Indels 3; Acodemy Conservative 0, Mismatches 8; Indels 3; Matches 2552; Conservative 0, Mismatches 8; Indels 3; Macches 2552; Conservative 10; Mismatches 10; Indels 10; Indel
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ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB88003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic cactivities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88257 represent primers and probes used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 ATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGGAAGCCAGTGCCTGTCATGTG 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rber H, Gerritsen ME, Goddard A;
Hillan KJ, Marsters SA, Pan J, Paoni NF;
Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
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2001US-00808689.
2001US-00816744.
2001US-00854208.
2001US-00854200.
2001US-00854280.
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2001US-00767609.
2001US-00796498.
2001WO-US006520.
2001WO-US006666.
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JF, Watanabe CK,
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28-FEB-2001;
28-FEB-2001;
01-MAR-2001;
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14-MAR-2001;
22-MAR-2001;
05-APR-2001;
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                                                                                                            2460 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTTGTTTTAAGTTGCTCAGTTTTGGTCT
                                                                                                                                                                                                                         AAGTTGTCTTTGTGA-CCAATAGGATATGGCAGAAGTGATGGCCATGCCACTTCCAAGATT
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                                                                                                                                                                             AAGTTGTCTTTGTGACCCAATAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATT
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20-JUL-2000; 2000US-0219556P.
25-JUL-2000; 2000US-022064P.
25-JUL-2000; 2000WS-0220664P.
28-JUL-2000; 2000WS-0220654P.
28-JUL-2000; 2000WS-0222695P.
17-AUG-2000; 2000US-0023657.
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07-SEP-2000; 2000US-0230978P.
18-SEP-2000; 2000US-00664610.
18-SEP-2000; 2000US-00665350.
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08-NOV-2000; 2000US-00709238
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1320 TGGGAGTANGGTGATTTTTCTTTTAAAATTAGGAGAGAATTACTGTGATTTTCTTTAATTTTTCTTTTAAAATTAGGAGAGATTATTCTTTTAAAATTAGGAGAGATTTTTCTTTTAAAAATTAGAAAGAA
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenois, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound
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                                                                                                                                                                                                                        Paoni NF;
                                                                                                                                                                                                                                                                                                       One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
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Pred. No. 0;
0; Mismatches 8; Indels 3;
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L, Hillan KJ, Marsters SA, Pan J,
CK, Williams PM, Wood WI, Ye W;
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Best Local Similarity 99.6%;
Matches 2552; Conservative
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JF, Watanabe CK,
 FERRARA N.
GERBER H.
GERRITSEN M E.
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STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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P-PSDB; ABB95580.
                                             GODDARD A.
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2436 TAAAGAGACTTAGGGGGAAAAAAATGAAGTCTCCTGCCCACAGCCACATTAGTGAACCTA 2495
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                                                          2496 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTTGTTGTTTTAAGTTGCTCAGTTTTTGGTCT
                                         GAAGCAGAGACTCTGTGAGATAATCGATGTTGTTGTTTTAAGTTGCTCAGTTTTGGTCT
                                                                                                              2556 AACTTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG 2598
                                                                                                 AACTTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG 2562
                                                                                                                                                                                                                                                                               Human angiogenesis related cDNA PRO4342 SEQ ID NO: 315.
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05-APR-2001; 2001US-00816366.
10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-0086628.
25-MAY-2001; 2001US-00866028.
25-MAY-2001; 2001US-00866034.
25-MAY-2001; 2001US-00866034.
25-MAY-2001; 2001US-0087097.
30-MAY-2001; 2001WG-US017092.
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2000WO-US032678.
2000US-00747259.
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2496 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTTTTTAAGTTGCTCAGTTTTGGTCT 2555
                                                                                                                                                          Human; ss; gene; secreted/transmembrane protein; PRO; tumour; cancer;
cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Godowski PJ;
                                                                                                                                             Human cDNA encoding secreted/transmembrane protein PRO4342
                                    2556 AACTIGITATGCAGCAATAGATAAATAATATGCAGAGAAAGAG 2598
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Wood WI;
                     2520 AACITGITAIGCAGCAAIAGAIAAAIAAIAIGCAGAGAAAGAG
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Watanabe CK,
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2001US-00816744.
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99US-00380137.
99US-00380138.
99US-00380142.
99US-00492397.
99US-00433344.
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99WO-US005028.
99US-00311832.
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Grimaldi JC, Gurney
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P-PSDB; ABO34010.
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08-NOV-2000; 2
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New isolated antibody specifically binding a PRO polypeptide, useful for the preparation of a medicament for treating disorders with the aberrant expression or activity of the PRO polypeptide, such as tumor conditions and cancer.

Disclosure; Fig 151; 223pp; English.

The invention relates to an antibody that binds to a secreted or transmembrane protein designated PRO1446 appearing as ABO33941. The protein is one of 84 PRO polypeptides which (along with their encoding nucleic acids) are disclosed in the specification. The methods and compositions of the present invention are useful for the preparation of amedicament for the treatment of disorders associated with the aberrant medicament for the treatment of disorders associated with the aberrant and cancer. They can also be used to generate transgenic or knockout animals useful in the development and screening of therapeutically useful reagents. The PRO polypeptides and encoding nucleic acids can be used as molecular weight markers for protein electrophoresis, chromosome identification and tissue typing. The antibodies may be used in various diagnostic, competitive binding and/or immunoprecipitation assays. The present sequence encodes a PRO polypeptide

Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;

457 540 120 TGAAGGACTCGGCATTGAAGGTGCTTTATCTGCATAATAACCAGCTTCTAGCTGGAGGGC 157 TGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGCGTGGTCCCCCAATCGGTGGCTGG 180 158 TGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGCGTGGTCCCCAATCGGTGGTGG 217 ATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGGAAGCCAGTGCCTGTCATGTG 240 ATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGGAAGCCAGTGCCTGTCATGTG 277 GGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 300 GGGIGGGGCAGGACCCGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 337 GTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGGACATGGGGCTCACCTCCAGCT 360 GTGCCAAGGAATCCCAAGAGCTTCACCTTCTACCGGCGGGACATGGGGCTCACCTCCCAGCT 397 TCGAGTCGGCTGCCTACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCTG 420 TCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACT 480 517 576 GTGAGGGGTGAGTGGAGGAGAGACCCCATGGCGGACAATCACTCTTTCTGCTCTCTCAGGACCCCC 600 636 999 CACGICIGACTIAGIGGGCACCIGACCACITIGIGGGTTCCCAGITIGGAIAAAIT 696 9 97 38 AGGGGAGTCTACACCCTGTGGAGCTCAAGATGGTCCTGAGTGGGGCGCTGTGCTTCCGAA 518 TCCAGCAGTGTGAGCCAACGTG-CCCCCAGAACTCCCTGGGCAGAGCCAGGG CAGGTCTGACTTAGTGGGCACCTGACCACTTTGTCTTCTGGTTCCCCAGTTTGCATAAATT TCAGACTCACCCAGCTTCCCGAGAATGGTGGTGGTAGTGCCCCCATCACAGACTTCTACT TCCAGCAGTGTGACTAGGGCAACGTGCCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGG TGAAGGACTCGGCATTGAAGGTGCTTTATCTGCATAATAACCAGCTTCTAGCTGGAGGGC TCGAGTCGGCTGCCTACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCTG AGGGGAGTCTACACCCTGTGGAGCTCAAGATGGTCCTGAGTGGGGCGCTGTGCTTCCGAA Gaps 3; Length 2598 8; Indels DB 8; Score 2514.2; Pred. No. 0; 0; Mismatches Query Match 98.1%; Best Local Similarity 99.6%; Matches 2552; Conservative 637 98 218 241 301 577 181 278 338 361 398 421 458 541 601 61 121 481 ઠે 셤 δ 셤 ઠે 셤 ð ద 8 ద ઠે 2 δ g ઠે 음 중 음 ò 요

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g &	81/ GIGGGGGGAAGIGGGAAAICAIICCIGCIIAAIGGIAACIGGAAAGIGIIACCCIGGAGCC 8/0
qa	877 CCGCAGGCCAACCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTC 936
& g	901 CTCTCACTCACCACTGTGCAGGAGGAGGTGGTCATAGAGTCAGGGATCTATGGCCCT 960
& 9	961 TGGCCCAGCCCCATCCCTTT-ATCCTGCACTGTATATGCTACCTTTCCTATC 1019
y da	1020 TCTTCCCTCATCATCTTGTGGGCATGAGGAGGTGGTGATGTCAGAAGAATGGTTCG 1079
Qy Pb	1080 AGCTCAGAAGATAAAGTAAGTAGGGTATGCTGATCCTCTTTAAAAACCCAAGATACA 1139
λο qa	40 ATCAAAATCCCAGATGCTGGTCTTATTCCCATGAAAAGTGCTCATGACATATTGAGAA 119
SP GS	00 GACCTACTTACAAAGTGGCATATATTGCAATTTATTTAATTAA
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& g	1320 TGGCAGTATAGGGGATTTTTCTTTTAATTCTGTTAATTTATCTGTATTTCCTAATTTTC 1379
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S G	1440 GAGCAGACATCATCTGATTGTCCTCAGCCTCCAATTCCCCAGAGTAAATTCAAATTGA 1499
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λο qg	1620 GAACAAAATCTGGTAATTCTTTCCTAGAAGGATCACAGCCCCTGGGATTCCAAGGC 1679
ඊ සි	1680 ATTGGATCCAGTCTCTAAGAAGGCTGCTGTTGGATTGTGTCCCCCTCAAATTCA 1739
ò	740 CATCCTTCTTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGCAGATGTAG 179

us-09-617-720a-1.rng

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The invention describes novel isolated PRO polypeptides. The PRO polypeptides or anti-PRO antibodies are useful in preparing a medicament contracting a condition that is responsive to the PRO polypeptide or antibody. The PRO nucleotide sequences may be used as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and probes in chromosome and gene mapping, or in generating antisense RNA and company to identify other proteins or molecules involved in binding reaction, to generate transgenic animals or knockout animals, which in the casents, for chromosome identification, and tissue typing. The PRO polypeptides and nucleic acid molecules are also useful in gene PRO polypeptides and nucleic acid molecules are also useful in gene PRO polypeptides and nucleic acid molecules are also useful in gene PRO polypeptides and nucleic acid molecules are also useful in gene PRO polypeptides and nucleic acid molecules are also useful in gene PRO, or for the affinity purification of PRO from recombinant cell PRO, or for the affinity purification of PRO from recombinant cell PRO, or for the affinity purification of PRO from recombinant cell purposes.
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AGGITATAAAAGACACIGCAGCITICTACITGAGCCCTCTCTCTCTGCCACCCCCCC
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New secreted and transmembrane PRO polypeptides and nucleic acid molecules encoding the polypeptides, useful in gene therapy or preparing a medicament for treating a condition that is responsive to the PRO

Disclosure; Fig 151; 409pp; English.

polypeptide or antibody.

Εζ,

Godowski

Goddard A, Wood WI;

Gerritsen ME, Watanabe CK,

Eaton DL, Filvaroff E, Grimaldi JC, Gurney AL,

2003-330984/31

P-PSDB; ABU72027

(GETH) GENENTECH INC

01-MAY-2002; 2002US-00063512 06-DEC-2001; 2001US-0006867

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23-JAN-2003

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Human; secreted and transmembrane polypeptide; gene; ss. chromosome mapping; gene mapping; transgenic animal; knockout animal; therapeutic agent screening; chromosome identification; tissue typing;

Homo sapiens gene therapy

Novel human secreted and transmembrane protein PRO4342 cDNA.

(first entry)

11-JUN-2003

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ACA60438 standard; cDNA; 2598

RESULT

337

240

ij,

Gaps

3,

8; Indels

Length 2598;

DB 8;

Score 2514.2; Pred. No. 0; 0; Mismatches

98.1%;

Local Similarity

Query Match

Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;

and transmembrane PRO poypeptide

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1500 ATCCAGCTCTGCTCTGCTCTGGTTGTTGTTGTTGTTGTGGAAACAGATCTCAGCAAACC 1556 1510 ATCCAGCTCTGCTCTGTGTTGTTGTTGTTGTTGTGAAACAGAAACAGAACTTCAAACAGAACTTAAA 1619 1591 ATCCAGCTCTGTGTGTTGTTGTTGTTGTTGTTGTATCTGGGAAACAGAACTTAAA 1619 1592 CACTGAGGAGGAGGGCTGTTGTTTGTTGTTGTTGTTGTTGTTGTGTTAAAAATTCTCTGGGAAATTCTTCAAGGAATTCAAAGAATTCTTTGTGTTAAAATTCTTCTGGGAATTCCAAGGC 1716 1601 ATTGGATCACTCTTGGTTAATTCTTTCCTAAAAATTCTTCTGGGAATTCCAAGGC 1716 1710 ATTGGATCACTCTTTGAAAATTCTTTCCTAAGAATTCTTCTGGGAATTCCAAGTC 1719 1710 ATTGGATCACTCTTTGAAAAGACTGTTGTTTTTTTGAAATTCTTTCT	TAAGAGACTTACGGGTAAAAATGAGGCCCCCCCCCCCCC
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Wood WI;
                                                                                            cDNA encoding human secreted polypeptide PRO4342
                                                                                                                  Human; 88; gene; gene therapy; tumour; cancer.
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Watanabe CK,
                         ACA58885 standard; cDNA; 2598 BP.
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99W0-US005028.
99W0-US010332.
99W0-US010733.
99US-00380137.
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22-AUG-2000; 2000US-00644848.
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28-FEB-2001; 2001WO-US006520.
22-MAR.2001; 2001US-00816744.
10-MAY-2001; 2001US-00854208
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18-SEP-2000; 2000US-0064610.
18-SEP-2000; 2000US-00665350.
08-NOV-2000; 2000US-00709238.
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02-MAR-2000; 2
21-MAR-2000; 2
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15-SEP-1999;
18-OCT-1999;
12-NOV-1999;
30-DEC-1999;
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                                                 ACA58885;
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Example 4; Page 220-221; 406pp; English.

Eaton

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tully defined sequence given in the specification. The methods and compositions (containing antibodies that specifically bind as PRO compositions (containing antibodies that specifically bind as PRO compositions (containing antibodies that specifically bind as PRO colypeptide) of the present invention are useful for the preparation of a medicament for the treatment of disorders associated with the aberrant can cancer. They can also be used to generate transgenic or knockout and cancer. The PRO polypeptide, such as tumour conditions can cancer. The PRO polypeptides and encoding nucleic acids can be used as molecular weight markers for protein electrophoresis, chromosome conditiotion and tissue typing. The PRO polypeptides are useful to induce angiogenesis e.g wound healing; in the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis diabetes; hyperinsulinaemia and hypoinsulinaemia. The arthritis diabetes; hyperinsulinaemia and hypoinsulinaemia. The immunoprecipitation assays. The present sequence represents a cDNA encoding a PRO polypeptide of the invention
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Matches 2552; Conservative
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TGAAGGACTCGGCATTGAAGGTGCTTTATCTGCATAATAACCAGCTTCTAGCTGGAGGGC
                                              ATGCCAGCCTGTCCCCGTCATCCTGGGTGTCCAGGGTGGAAGCCAGTGCCTGTCATGTG
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Wood WI;
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Pred. No. 0;
0; Mismatches
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Watanabe CK,
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2000WG-US023328.
2000WG-US023328.
2000US-00664510.
2000US-00664510.
2000US-00709238.
2000WG-US032678.
2000WG-US032678.
99WO-US005028.
99US-00311832.
99US-00380133.
99US-00380138.
99US-00380139.
99US-00380142.
99US-00403297.
99US-00403297.
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2000WO-US007532.
2000WO-US014042.
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22-MAR-2001, 2001US-00816744.
10-MAY-2001, 2001US-00854208.
10-MAY-2001, 2001US-00854208.
30-MAY-2001, 2001US-00870574.
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29-JUN-2001; 2001US-00869599.
18-JUL-2001; 2001US-00908827.
06-DEC-2001; 2001US-00006867.
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Best Local Similarity 99.6%;
Matches 2552; Conservative
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P-PSDB; ABU72362
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28-FEB-2001; 2
22-MAR-2001; 2
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25-AUG-1999;
25-AUG-1999;
15-SEP-1999;
18-OCT-1999;
12-NOV-1999;
13-DEC-1999;
18-FEB-2000;
01-MAR-2000;
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22-MAY-2000;
02-JUN-2000;
22-AUG-2000;
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18-SEP-2000;
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Grimaldi JC,
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lung; stomach; oesophageal; skin; tumour; cancer; cytostatic;
gene therapy; gene; ss.
CAATCTATCTTGGCTCACTCGCTCTGGGGGAAGCTAGCTGCCATGCTATGAGCAGGCCTA
                                                                                                                                                              TAAAGAGACTTACGTGGTAAAAATGAAGTCTCCTGCCCACACGCCACATTAGTGAACCTA
                                                                                                                                                                                TABABGBGACTTACGTGGTAAAAATGAAGTCTCCTGCCCACAGCCACATTAGTGAACTA
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25-AUG-1999; 9US-00380137.
25-AUG-1999; 9US-00380137.
25-AUG-1999; 9US-00380139.
25-AUG-1999; 9US-00380139.
25-AUG-1999; 9US-00380142.
15-SEP-1999; 9US-0039742.
12-NOV-1999; 9US-0042344.
30-DEC-1999; 9US-0042344.
30-DEC-1999; 9US-0043274.
18-FEB-2000; 2000WO-US005841.
21-MAR-2000; 2000WO-US005841.
21-MAR-2000; 2000WO-US005841.
22-MAR-2000; 2000WO-US015841.
22-MAR-2000; 2000WO-US015841.
22-MAR-2000; 2000WO-US015841.
24-AUG-2000; 2000WO-US015841.
24-AUG-2000; 2000WC-US015841.
24-AUG-2000; 2000WC-US015873.
18-SEP-2000; 2000WS-00664610.
18-SEP-2000; 2000WS-00664610.
18-SEP-2000; 2000WS-00664610.
18-SEP-2000; 2000WS-00664610.
20-DEC-2000; 2000WS-0US0134956.
22-MAR-2001; 2001WS-0US014956.
22-MAR-2001; 2001WS-0US014956.
22-MAR-2001; 2001WS-0US014956.
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99WO-US005028.
99WO-US01033.
99US-00380137.
99US-00380138.
99US-00380142.
99US-00397342.
99US-00403297.
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Pred. No. 0;
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10-MAY-2001; 2001US-00854280.
30-MAY-2001; 2001US-00870574.
01-JUN-2001; 2001US-00874503.
05-JUN-2001; 2001US-00874503.
29-JUN-2001; 2001US-0086959.
18-JUL-2001; 2001US-00908827.
06-DEC-2001; 2001US-00006867.
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99.6%;
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Matches 2552; Conservative
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                                                                                                                                                                                                     (GETH ) GENENTECH INC
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Human; 88; tumour; cancer; gene therapy; tissue typing;
                 Human secreted/transmembrane polypeptide PRO4342
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standard; cDNA; 2598

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ACD45224 ID ACD4 XX AC ACD4 XX

ACD45224

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New isolated antibody specifically binding a PRO polypeptide, useful for the preparation of a medicament for treating disorders with the aberrant expression or activity of the PRO polypeptide, such as tumor conditions and cancer.
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18-SEP-2000; 2000US-00664610.
18-SEP-2000; 2000US-00665350.
10-NOV-2000; 2000W0-US032678.
20-DEC-2000; 2000W0-US032678.
20-DEC-2000; 2000W0-US032678.
20-DEC-2000; 2000W0-US032678.
20-DEC-2000; 2000W0-US03650.
28-FEB-2001; 2001W0-US034956.
28-FEB-2001; 2001W2-0081674.
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99WO-US005028.
99WO-US01033.
99US-00380137.
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06-DEC-2001; 2001US-00006867.
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2000WO-US023328.
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01-JUN-2001; 2001WO-US017800.
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P-PSDB; ABO27356.
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15-SEP-1999;
18-007-1999;
30-DEC-1999;
18-FEB-2000;
01-MAR-2000;
02-MAR-2000;
21-MAR-2000;
22-MAY-2000;
22-MAY-2000;
22-AUG-2000;
24-AUG-2000;
Homo sapiens.
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Grimaldi JC,
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901 CTCTCACTCACCACTGCAGGAGAGGAGGTCATAGAGTCAGGGATCTATGGCCCT 960 917 CTGTCACTCACCACTGTGCAGGAGGGGGGGTCATAGAGGATCTATGGCCCT 960 918 TGGCCAGCCCACCCCTTCCCTTT-ATCCTGCCACTGCATATGCTCATTCTATTGCTCT 101 919 TGGCCCAGCCCCACCCCTTCCTTT-ATCCTGCCATCATATGCTACTTTCCTATC 105 910 TGGCCCAGCCCCACCCCTTCCTTTTAATCCTGCCATCATATGCTACTTTTCTATT 105 1020 TGGCCCAGCCCCCTTTGTTGTGGGCATGAGGGTCATAGTTCTG 107 1057 TCTTCCCTCATCATTGTTGTGGGCATGAGGGGTGATGTTGTG 107 1057 TCTTCCCTCATCATTGTTGTTGTGGGATGAGGGTGATGTTGT 113 1080 ÀGCTCAGAAGATAAAAGATAGGGTGATGCTGATTTTAAAAAACCCCAAGATACA 113 1117 AGCTCAGAAGATAAAGATAGGGTATGCTGATTCTTTTAAAAACCCCAAGATACA 113 1117 AGCTCAGAAGATAAAGATAGGTATGCTGATCCTCTTTTAAAAACCCCAAGATACA 113	1140 ATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAGTGCTCATGACATATTGAGAA 1199 1177 ATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGCTCATGACATATTGAGAA 1236 1200 GACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAATTAA	TGGCAGTATAGGTGATTTTTCTTTTAATTCTGTTAATTTATCTGTATTTCCTAATTTTTC	1477 GAGCAGACATCATCTCTGATTGTCCTCAGCCTCCCCCAGAGTAAATTCAAATTGA 153 1500 ATCGAGCTCTGCTCTCGTTGGTTGTAGTAGTAATCAGAAACAGAAACAGAACTCAGCAAAGC 155: 1537 ATCGAGCTCTGCTCTCTGGTTGTTGTAGTAGTAGTCAGGAAACAGATCTCAGCAAAGC 159: 1560 CACTGAGGAGGCTGTCTCTGGTTTGTTGTGTGGGAATCTCTGGGATAGGAACTTAAA 161: 1597 CACTGAGGAGGCTGTGCTGAGTTTGTGTGTGGCTGGAATCTCTGGGTAAGGAACTTAAA 161: 1597 CACTGAGGAGGAGGTGTGCTGAGTTTGTGTGTGCTGGAATCTCTGGGTAAGGAACTTAAA 165: 1620 GAACAAAAATCATCTGGTAATTCTTTCCTAGAAGGATCTCTGGGTAAGGAACTTAAA 165:	7 GAACAAAATCATCTGGTAATTCTTTCCTAGAAGGATCACAGCCCCTGGGATTCCAAGGC ATTGGATCCACTGGTAATTCTTTCCTAGAAGGATCACAGGCCCTGGGATTCCAAGGC ATTGGATCCACTCTTAAGAAGGCTGCTGTACTGGTTGAATTGTGTCCCCCTCAAATTCA	1800 TTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTCAATATGACTGGTTTCC 185 1837 TTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTCAATATGACTGGTTTTCC 189 1860 TTGTATGAAAAGGACACGTGAACGAGACAGAGACCTAAATTCAATATGACTGGTTTTCC 189 1870 TTGTATGAAAAGGACACACAGAGACAGAGAGACGCGGGGAAGACTATGTAAAGATG 191 1891 TTGTATGAAAAGGAGAACACAGAGACAAGAGACGAGGAAGACTATGTAAAGATG 195 1920 AAGGCAGAGATTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACCA 197 1951 AAGGCAGAGATTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACCA 197 1952 AAGGCAGAGATTTTTTTTTTTTTTTTTTTTTTTTTTTTT
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15-SEP-1999;
18-OCT-1999;
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02-MAR-2000;
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                                                                                                                                                                                                                                                                                        Grimaldi
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; 88; gene; PRO; secreted protein; transmembrane protein; cytostatic; vulnerary; osteopathic; antiarthritic; antirheumanic; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tumour necrosis factor; pericyte cell proliferation; TNF-alpha; proteoglycans release; cartilage; cancer; wound healing; cartilage defect; osteoarthritis; rheumatoid arthritis.
TAAAAGAGACTTACGTGGTAAAAAAATGAAGTCTCCTGCCCACAGCCACATTAGTGAACCTA
                                           CTGTTTTAAGCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAAACTAATACAGCTGCT
                                                                                                              AAAATGATCCCTGTCTCCTGTTTTACATTCTGTGTGTGTCCCCTCCCACAATGTACCA
                                                                                                                              AAGTTGTCTTTGTGACCCAATAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATT
                                                                                                                                               AAGTTGTCTTTGTGA-CCAATAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATT
                                                                                                                                                                 CAATCTATCTTGGCTCACTCGCTCTGGGGGAAGCTAGCTGCCATGCTATGAGCAGGCCTA
                                                                                                                                                                                                                                     TAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCTGCCCACAGCCACATTAGTGAACCTA
                                                                                                                                                                                                                                                                       GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTTTTTAAGTTGCTCAGTTTTGGTCT
                                                                                                                                                                                                                                                                                 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTTTTAAGTTGCTCAGTTTTGGCCT
                                                            CTGTTTTAAGCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAAACTAATACAGCTGCT
                                                                                             AAAATGATCCCTGT:CTCCTCGTGTTTACATTCTGTGTGTGTCCCCTCCCACAATGTACCA
                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA encoding secreted/transmembrane protein PRO4342
                                                                                                                                                                                                                                                                                                         AACTIGITATGCAGCAATAGATAAATAATATGCAGAGAAGAG 2562
                                                                                                                                                                                                                                                                                                                  AACTIGITATGCAGCAATAGATAAATATGCAGAGAAAGAG
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99WO-US055028.
99WG-0311832.
99WG-US010733.
99US-00380137.
99US-00380138.
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25-AUG-1999;
25-AUG-1999;
25-AUG-1999;
25-AUG-1999;
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08-MAR-1999;
14-MAY-1999;
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The invention relates to a new isolated PR0994 polypeptide comprises an amino acid sequence appearing as ABU92499, PR0994 lacking its associated signal peptide, the extracellular domain of PR0994, the extracellular domain of PR0994, the extracellular domain of PR0994 (lacking it associated signal peptide) or the protein encoded by the full-length coding sequence of the cDNA ATCC 203018. Also included is a chimaeric molecule comprising the PR0994 polypeptide fused to a heterologous amino acid sequence. The PRO polypeptide is useful in pharmaceuticals, diagnostics, biosensors or bioreactors. It is particularly useful for detecting tummours (e.g. lung tummour, colon tummour, breast tummour, prostate tummour, rectal tummour, or liver tummour) in a mammal, for stimulating the release of tummour necrosis factor (TNF) alpha from human blood, for stimulating the proliferation of pericyte cells, or stimulating the release of proteoglycans from cartilage. The polypeptide may be employed for a variety of therapeutic purposes, e.g. for treating cancer, wound healing, cartilage defects, osteoarthitis, theumatoid arthritis. Also disclosed are the cDNA encoding PR0994, 83 other PRO polypeptides and their encoding cDNAs. The present sequence encoding a PRO polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 AGGGGAGTCTACACCCTGTGGAGCTCAAGATGGTCCTGAGTGGGGCGCTGTGCTTCCGAA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New PRO994 polypeptide, useful for detecting tumors, or for stimulating tumor Necrosis Factor alpha, or pericyte proliferation, especially for treating cancer, cartilage defects, osteoarthritis and rheumatoid arthritis in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGGGAGTCTACACCCTGTGGAGCTCAAGATGGTCCTGAGTGGGGCGCTGTGCTTCCGAA
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Wood WI;
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Pred. No. 0;
0; Mismatches
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Watanabe CK,
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                                                                                                                                                                             2000US-00644848.
2000WO-US023328.
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2000US-00665350.
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2000US-00747259.
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2001WO-US006520.
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2001US-00854208.
2001US-00854280.
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2000WO-US004341
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2001WO-US017800
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Matches 2552; Conservative
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Best Local Similarity
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18-SEP-2000;
08-NOV-2000;
10-NOV-2000;
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1140 ATCARANTCCCAGATGCTGGTCTGTTTCCCATGAAAAGTGCTCATGACATTTGAGA 1136	1860 TTGTATGAAAGGAGACACAGACACAGAGACGCGGGGAAGACTATGTAAAGATG 1919 1897 TTGTATGAAAGGAGACACAGACACAGAGACGCGGGGAAGACTATGTAAAGATG 1919 1897 TTGTATGAAAAGGAGACACAGGACACAGGAGACACACAGGATTGTAGAAGATG 1956 1950 AAGGCAGAAAAAGGATTTTGCAGCCACAGGATTGTTGGCAACCA 1979 1951 AAAATGATCGGAGATTTTGCAGCCACAGGATTGTTGGCAACCA 1979 1951 AAAATGATCACAGAAGAAGAATTCTTCCCTAGAGGATTGTGGCAACCA 2016 1960 TCAGAAGCTTGGAAGAGAAGAATTCTTCCCTAGAGGATTAGAGGATAACGGC 2039 2017 TCAGAAGCTTGGAAGAGAAGAATTCTTCCCTAGAGGATTAGAGGATAACGGC 2076 2040 TCTGGTGAAACCTTAATCTCAGACATCCCTGAAGGAATAAATTTCGG 2039 2077 TCTGGTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAAGAAAAAAATTTCGG 2136 2077 TCTGCTGAAACCTTAATCTCAGACTTACAGCTCTCTGAAGAAAAAAAA
8 4 8 4 8 4 8 4 8 4 8 4 8 4 8 4 8 4 8 4	6 B 6 B 6 B 6 B 6 B 6
TGAAGGACTCGGCATTGAAGGTGCTTTATCTGCATAATAACCAGCTTCTAGCTGGAGGGC	GTGGGGGAGTGCTGGGAATCATTCCTGCTTAATGGTAACTGACAAGTGTTACCCTGAGCC 87 GTGGGGGAGTGCTGGGAATCATTCCTGCTTAATGGTAACTGACAAGTGTTACCCTGAGCC 87 GTGGGGGAGTGCTGGGAATCATTCCTGCTTAATGGTAACTGACAAGTGTTACCCTGAGCC 87 CCGCAGGCCAACCCCATCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCCACATGAAGTC 90 CCGCAGGCCAACCCATCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCCACATGAAGTC 90 CCGCAGGCCAACCCATCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCCACATGAAGTC 90 CCGCAGGCCAACCCATCCCATTAATGGTCATAGAGTCAGGAATCTATGGCCCT 96 CTGCCCAGCCCCACCCCCTTCCCTTTAATCCTGCCACTAGAGTCAAGGAATCCTATCCTATC 10 TGGCCCAGCCCCACCCCCTTCCCTTTAATCCTGCCACTGTCATAGCTCCTTTCCTATC 10 TCGCCCAGCCCCACCCCCTTCCTTTAATCCTGCCACTGTCAAAGAATCCTTCTTTCT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an antibody that binds to a secreted and transmembrane polypeptide, PRO1136. The antibody is useful for preparing a medicament useful in the treatment of a condition responsive to anti-PRO antibody. The antibody is also useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. The present sequence represents a cDNA encoding a PRO polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                               New monoclonal antibody that binds to a secreted and transmembrane polypeptide, useful for detecting and purifying the polypeptide and also for treating conditions responsive to the antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGGAAGCCAGTGCCTGTCATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGCCAGCCTGTCCCCCCGTCATCCTGGGTGTCAGGTGGAAGCCAGTGCCTGTCATGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGACTCCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACT
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                                                                                                                                                                                                                          Ρ.
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                                                                                                                                                                                                                          Godowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;
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Wood WI;
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                                                                                                                                                                                                                          Gerritsen ME,
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Fig 151; 235pp; English
10-MAY-2001; 2001US-00854208.

10-MAY-2001; 2001US-00854280.

30-MAY-2001; 2001US-00870574.

01-JUN-2001; 2001US-00874503.

05-JUN-2001; 2001US-00869599.

18-JUL-2001; 2001US-00968827.

06-DEC-2001; 2001US-00006867.
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                                                                                                                                                                                  (GETH ) GENENTECH INC
                                                                                                                                                                                                                          Filvaroff
                                                                                                                                                                                                                                               Gurney
                                                                                                                                                                                                                                                                                  WPI; 2003-341840/32.
P-PSDB; ABU81221.
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                                                                                                                                                                                                                          Eaton DL, Fil
Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
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 and transmembrane protein PRO4342 cDNA.
                               88
                               Human; secreted and transmembrane protein; PRO; gene;
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Wood WI;
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Watanabe CK,
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99WO-US005028.
99WO-US010133.
99US-00380137.
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99US-00397342.
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Grimaldi JC, Gurney AL,
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human secreted
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18-OCT-1999;
10-NOV-1999;
10-PER-2000;
01-MAR-2000;
22-MAR-2000;
22-MAR-2000;
22-MAY-2000;
22-AUG-2000;
24-AUG-2000;
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                                                             Homo sapiens
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AI167887	AK009741	AK008977	AU157708	CB590160	AK014576	CB589411	CR742272	AK010020	BY709379	BG010066	R70041	AY413264	R70089	BX477358	CB194288	BY754693	BY708859	W08205	AW014217	CC526753
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387.4	384.6	384.6	380.8	379.8	379.4	373.4	367	366.6	360	349.6	349.4	327	315.4	300	271.4	263	257.4	227.2	222.4	216.8
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ALIGNMENTS

CR613851
LOCUS CR61381 2605 bp mRNA linear HTC 21-JUL-2004 DEFINITION full-length DNA clone CSODI013YA07 of Placenta Cot 25-normalized of Homo sapiens (human).
NOI NO N
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minidae;
II E
JOURNAL Unpublished REMARK Contact : Forth initial : fliang@lifetech.com URL :
REFERENCE 2 (bases 1 to 2605) AUTHORS Genoscope.
Direct Submission
COMMENT 1st strand cDNA was primed with a NotI-011go (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned the control to the the test of the control of the contro
and the not 1 and book v sicks of the purvisions o vector. Dibiary was normalized. Library was constructed by Life Technologies, a
FEATURES Location/Qualifiers source 12605
/organism="Homo sapiens" /mol type="mRNA"
/db_xref="taxon:9606" /clone="CSOD1013YA07"
/tissue type="Placenta Cot 25-normalized" / plasmid="pcMVSPORT 6"
ORIGIN
Query Match 96.3%; Score 2469.2; DB 3; Length 2605; Best Local Similarity 99.2%; Pred. No. 0;
vative 0
Oy 1 AGGGAGTCTACACCCTGTGGAGCTCAAGATGGTCCTGAGTGGGGCGCTGTGCTTCCGAA 60

1140 ATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAGTGCTCATGACATATTGAGAA 1199	1410	1620 GAACAAAAATCATCTGGTAATTCTTTCCTAGAAGGATCACAGCCCTGGGATTCCAAGGC 1679 1693 GAACAAAAATCATCTGGTAATTCTTTCCTAGAAGGATCACAGCCCCTGGGATTCCAAGGC 1752 1680 ATTGGATCCAGTCTTAAGAAGGCTGCTACTAGTTGAATTGTGTCCCCCTCAAATTCA 1739 1753 ATTGGATCCAGTCTCTAAGAAGGCTGCTGACTGGTTGAATTGTGTCCCCCTCAAATTCA 1812 1740 CATCCTTCTTGGAATCTCAGTCTGGAGTTTATTTGGAGATAAGGTCTCTGCAGATGTAG 1799 1740 CATCCTTCTTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAAGGTCTCTGCAGATGTAG 1799	TTAGTTAAGACAAGGTCATGCAGATGAAGGTAGACCTAAATTCAATATCAGTTTCC	80 53 40 00 00 60 60
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 3 Row: i Column: 18 This clone has the following problem: retained intron. Location/Qualifiers
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181 GATACAATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGCTCTGTGATAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1254 TITATATATITCTITATAGAAAAAGICTGGAAGAGITIACTICAATIGTAGCAATGTA 1313
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Center
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: angobcm.tmc.edu
Contact: angobcm.tmc.edu
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Loulseged, H.,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAGCAGAGCAGACATCATCTCTGATTGTCCTCAGCCTCCAATTCCCCAGAGTAAATTCA 1493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 1648;
                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/do_tref="taxon:9606"
/clone="INAGE:3447369"
/tissue_type="Placenta, choriocarcinoma"
/clone=Iib="NIH MGC_10"
/lab_hoste="DH108"
/note="Vector: pCMV-SPORT6"
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Pred. No. 0;
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Matches 1597; Conservative (
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1. (bases 1 to 1648)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N. K., Hopkins, R.F., Jordan, H., Moore, T.A., Rarmer, R.J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helten, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.B., Schein, J.B., Jones, S.J. and Marra, M.A.
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Homo sapiens interleukin 1 family, member 5 (delta), mRNA (CDNA clone IMAGE:3447369), with apparent retained intron.
BC000945
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                                                                          AGGITATAAAAGACACIGCAGCITCTACITGAGCCCTCTCTCTGCCACCCACCGCCCC 2339
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                           AAGTTGTCTTTGTGA-CCAATAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATT 2351
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Direct Submission
Submitted (16-NOV-2000) National Institutes of Health, Mammalian
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2599,
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NIH-MGC Project URL: http://mgc.nci.nih.gov
On Jul 12, 2001 this sequence version replaced gi:13937574.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: APCC
CDNA Library Preparation: Life Technologies, Inc.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRV cedex - FRANCE
Email: sequencope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster

For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI013AA04NP1&c=1383.f. Location/Qualifiers

1383.£

organism="Homo sapiens"

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

sapiens

gi:31292372

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length CDNA libraries and normalization
Unpublished (2001)
Feb 16, 2001 this sequence version replaced (
Contact: Genoscope

us-09-617-720a-1.rst

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                                                                                                                                                    961 AAGATGAAGGCAGAGTTCTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGG
              1560 TGGTCTAACTTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAAGAGA 1609
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                                                                                                                                             954 AIGAGTIGIGGGGGGGAACTCTGGGTAAGGAACTIAAAGAACAAAATCATGGGTA
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                                                               GTTGGTTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTG
                               Gaps
                               5
 Length 1140;
                                 Indels
Score 980.2; DB 1;
Pred. No. 3.2e-242;
3; Mismatches 6;
    38.2%;
                     Best Local Similario,
Matches 1004; Conservative
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AL570964
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1818

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1638

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GI:46237085

AL570964.3

RESULT 3 AL570964/c LOCUS DEFINITION ACCESSION VERSION

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/gex="male"
/dev stage="newborn infant"
/lab host="E. coli SOLR"
/lab host="E. coli SOLR"
/clone lib="Katze MMPL2"
/clone
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                                                                                                                                                                                                                                                                       Length 1080
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                                                                                                                                                                                                                                                                     Query Match 28.5%; Score 731.6; DB 7; Best Local Similarity 89.6%; Pred. No. 7.8e-178; Matches 833; Conservative 0; Mismatches 89;
     'db_xref="taxon:9544"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CK232552 1080 bp mRNA linear EST 09-DEC-2003 ILLUMIGEN MCQ 4234 Katze_MMPL2 Macaca mulatta cDNA 5' similar to human ILLF5 (H8.207224), mRNA sequence.
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1 (bases 1 to 1080)

Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L. Large-scale Rheemus Macaque cDNA Sequencing
Unpublished (2003)

Contact: C. Magness
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                                                                            2059 CAGACTTCCAGCCTCCTGAACGAAGAATAAATTTCGGCTGTTTTAAGCCACCAAGG
                                                                                                        474 CAGACTICCAGCCTCCTGAACGAAGAATAAATITTCGGCTGTTTTAAGCCACCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cmagness@illumigen.com
Sequenced on 2003.12.02. 777 Q20 bases. Assemb
member(s). Contig contains 1 (0%) lib members.
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2203 Airport Way S, Suite 450, Seattle,
Tel: 2063780400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR PRIMERS
FORWARD: CCCTCACTAAAGGGAACAAA
FORWARD: CACTATAGGGCGAATTGGGTA
INSERT LENGTH: 1080 Std Error: 0.00
Plate: CL000050 row: B column: 10
Seg primer: CCCTCACTAAAGGGAACAAAA

    .1080
    /organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"

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Macaca mulatta
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AUTHORS
TITLE
JOURNAL
COMMENT
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I (bases 1 to 750)

Ebert, L., Helni, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Human UnigeneSet - RZPD3

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAACAGCTATGAC.
Location/Qualifiers
1. 750
                                                                                                                                                                                                                                                                                                                                                554 TCCAGCAGTGTGACTAGGGCAACGTG-CCCCCAGAACTCCCTGGGCAGAGCCAGCTCGG
                                                                                                                                                               434 TCGAGTCGGCTGCCTACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCTG
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                           GTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGACATGGGGCTCACCTCCAGCT
                                                       374 GIGCCAAGGAAICCAAGAGCIICACCIICTACCGGGGGGACAIGGGGCICACCICCAGCI
                                                                                                                                                                                                                      421 TCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCCATCACAGACTTCTACT
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                                                                                                                         TCGAGTCGGCTGCCTACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCTG
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RZPDIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB NO.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response7libNo=972 Contact: Ina Rolfs
bin/showLib.pl.cgi/response7libNo=972 Contact
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BX091500 Thoear SSI Pp mRNA linear ESI BX091500 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGP998H07211 ; IMAGE:142518, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BX091500.1 GI:27822499
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr |
1st strand cDNA was ptimed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSDRT & vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                      EST 25-MAR-2004
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AL545100 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens CDNA Clone (SSD1013YA07 5-PRIME, mRNA sequence.
AL545100
841 GTCTCCTCGTGTGTTCACATTCTGTGTGTATCCCCTCCCCAATGTACCAGAGTTGGTCTTCC 900
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo (dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 985)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31266936.
Contact: Genoscope
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Catarrhini; Hominidae; Homo
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Pred. No. 6.4e-173;
4; Mismatches 18;
                                                                                             901 TGACTAATAAATAATGCCAAAAGTGATGG 930
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                                                TGACCCAATAGAATATGGCAGAAGTGATGG
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/db_xref="taxon:9606"
/clone="CS0DI013YA07"
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Mammalia; Eutheria; Primates;
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larity 96.5%;
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Library prepared by Life
Technologies."
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S NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs.remail.nih.gov

Tissue Procurement: Arco

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Incyte Genomics, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llh.gov

Plate: LLAM11021 row: n column: 17

High quality sequence stop: 709.

Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 726)
                                                                                                           BI089828 1726 bp. mRNA linear EST 20-JUN-20
602855071F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4996432 5',
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Pred. No. 1.7e-165;
0; Mismatches 12;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/cell_line="MGC36"
/lab_host="DH108"
                                                                                                                                                    mRNA sequence. _ _ BI089828
BI089828.1 GI:14508158
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al Similarity 98.1%;
713; Conservative (
719 TGCAGAGAAGAGA 732
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2070 CCTCCTGAACGAAGAATAAATTTCGGCTGTTTTAAGCCACCAAGGATAATTGGTTA 2129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCAGCTCTAGGAAACTAATACAGCTGCTAAAATGATCCCTGTCTCCTCGTGTTTACAT 2189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2250 CAGAAGTGATGCCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTCTACTT 2309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2490 TIGITGITITAAGITGCTCAGITITTGGTCTAACTTGTTATGCAGCAATAGATAAATAATA 2549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTAGACCTAAATT-AATATGACTGGTTTCCTTGTATGAAAAGGAGAGACACAGAGACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 CAGCAGCTCTAGGAAACTAATACAGCTGCTAAAATGATCCCCTGTCTCCTCGTGTTTACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCCTGCCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 27.6%; Score 707; DB 5; Length 750; Best Local Similarity 99.3%; Pred. No. 1.7e-171; Matches 729; Conservative 0; Mismatches 3; Indels
                                                                 clone="IMAGp998H07211 ; IMAGE:142518"
  sapiens"
                  Lype="mRNA"
xref="taxon:9606"
'organi.sm="Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 1. 702 | Accasion | 
                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mamaalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 702)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Ganer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from Dr. M. Bento Soares, bento-soares@ulowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-61, AT_rich#Low_complexity
Seq primer: MI3 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Human Lung Alveolar Macrophage
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TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                         ORGANISM
                                                                                                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                    JOURNAL
COMMENT
                                                                                                                REFERENCE
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697 bp mRNA linear EST 06-DEC-2000
UI-H-BI4-aou-e-01-0-UI.sl NCI_CGAP_Sub8 Homo sapiens cDNA clone
IMAGE:3086280 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGATCTATGGCCCTTGGCCCCAGCCCCTTCCCTTT-ATCCTGCCACTGTCATATG 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTACCTTTCCTATCTTCCTCATCATCTTGTTGTGGGCATGAGGTGGTGATGTCA 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1126 AAACCCAAGATACAATCCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAGTGCTCA 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                            224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 GAAGAAATGGCTCGAGCTCCAGAAGATAAAGATAAGTAGGGGTATGCTGATCCTCTTTTAA 164
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                                                                                                                                                                                                                                                                                                                                                                                   TGTTACCCTGAGCCCCGCAGGCCAACCCATCCCCAGTTGAGGCCTTATAGGGTCAGTAGCT 404
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 697)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-GAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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www-bio.llnl.gov/bbrp/image/image.html The following repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 CTACCTTTCCTATCTTTCCTTCATCATCTTGTGGGCATGAGGAGGTGCTGATGTCA
702 GCTCTCAGGACCCCCACGTCTGACTTAGTGGGCACCTGACCACTTTGTCTTCTGGTTCCC
                                                 AGTTTGCATAAATTCTGAGATTTGGAGCTCAGTCCAGGGTCCTCCCCCACTGGATGGTGC
                                                                                                                                                                                        583 TACTGCTGTGGATCTTGTAANAACCATGTGGGGTAAACTGGGGATAACATGAAAAGATT
                                                                                                                                                                                                                                        TCTGTGGGGGGGGGGGGGGGGGGGGAATCATTCCTGCTTAATGGTAACTGACAAG
                                                                          TACTGCTGTGGAACCTTGTAAAAACCATGTGGGGTAAACTGGGAATAACATGAAAAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTACCCTGAGCCCCGCAAGCCAACCCAGTTGAGCCTTATAGGGTCAGTAGCT
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BF509095.1 GI:11592393
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Unpublished (1997)
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Homo sapiens
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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Query Match 25.2%; Score 644.6; DB 6; Length 702; Best Local Similarity 97.4%; Pred. No. 2.4e-155; Matches 675; Conservative 0; Mismatches 16; Indels 2

Gaps

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1130 CCAAGATACAATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAGTGCTCATGAC 1189
                                                                                                                                                       858 bp mRNA linear EST 20-JUN-2001
60285574F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4996939 5',
BI090567
218 AAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAAC 159
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Library prepared by Life
                                                                                   158 CCAAGATACAATCACAAAATCCCAGATGCTGGTCTTATTCCCATGAAAAGTGCTCATGAC 99
                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherita; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 858)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llni.gov c column: 20
Plate: LiAM11023 row: c column: 20
High quality sequence stop: 670.
Location/Qualifiers

1. 858
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                                                                                                                                                                                                                                                             CCTATITATATITICITITATAGAAAAA 1278
                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:4996939"
/cell_line="MGC36"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI090567.1 GI:14508897
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Homo sapiens
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                                                                                                                                                                                                                                                                          /done lib="NOT GAPE Sub8"
/clone lib="NOT GAPE Sub8"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco Ri; NCI CGAP Sub8
is a subtracted library derived from NCI CGAP Sub8
is a subtracted library derived from NCI CGAP Sub8
is a subtracted library had 2.5 million recombinants. A
single-stranded DNA preparation of NCI CGAP Sub5 The
NCI CGAP Sub8 library had 2.5 million recombinants. A
single-stranded DNA preparation of NCI CGAP Sub5 (IMAGE
comprising: a pool of clones from NCI CGAP Sub5 (IMAGE
clone Ids 2732833-2733415, 306840-306919; 25% of the
driver population), apool of clones from NCI CGAP Sub4
(INAGE clone Ids 2723522-2723325; 25% of the driver
population), NCI CGAP Sub6 (pool AIF-AJU, IMAGE Ids
2728969-27313190; 25% of the driver population), and
NCI CGAP Sub7 (IMAGE Ids 3069192-3072238,
3081864-3084550; 25% of the driver population),
Subtraction was performed as previously described
[Bonaldo, Lemnon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery.
GGAOME Research 6, 791-806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 951 CTATGGCCCTTGGCCCCAGCCCCCTTCCCTTT-ATCCTGCCACTGTCATATGCTAC 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1010 CTTTCCTATCTCTCCCTCATCATCTTGTTGGGCATGAGGAGGTGGTGATGTCAGAAG 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1070 AAATGGTTCGAGCTCAGAAGATAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAAC 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         651 IGCATAAATTCTGAGATTTGGAGCTCAGTCCACGGGTCCTCCCCCACTGGATGGTGCTACT 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        591 TCAGGACCCCCCAGGTCTGACTTAGTGGGCACCTGACCACTTTGTCTTCTGGTTCCCAGTT 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     697 TCAGGACCCCCACGTCTGACTTAGTGGGCACCTGACCACTTTGTCTTCTGGTTCCCAGTN 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             578 GCTGTGGAATCTTGTAAAACCATGTGGGGTAAACTGGGAATAACATGAAAAGATTTCTG 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518 TGGAGGTGGGGTGGGGGAGTGGTGGGAATCATTCCTGCTTAATGGTAACTGACCAGTGTT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          458 ACCCTGAGCCCCGCAGGCCAACCCATCCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACATGAAGTCCTCTCACTCACCACTGTGCAGGAGAGAGGAGGTGGTCATAGAGTCAGGGAT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398 ACATGAAGACCTGTCACTCACCACTATGCAGGAGGAGGAGGGGGGTGGTCATAGAGTCAGGGAT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338 CTATGGCCCTTGGCCCAGCCCACCTCCTTCCCTTTAATCCTGCCACTGTCATATGCTAC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGTGGAACCTTGTAAAACCATGTGGGGTAAACTGGGAATAACATGAAAAGATTTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCCTGAGCCCCGCAGGCCAACCCATCCCCAGTTGAGGCCTTATAGGGTCAGTAGCTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         637 IGGATAAATTCIGAGATTT-GAGCTCAGTCCACGGTCCTCCCCCACTGGATGGTGCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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  elements were found in this cDNA sequence: 1-60,
                                                                                                                                                                                                                                                             /lab_host="DH10B (Life Technologies)"
                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3086280"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAG_TISSUE=lung
TAG_LIB=NCI_CGAP_Lu19
TAG_SEQ=GACAGC"
                                                                                                      Location/Qualifiers
                >AT_rich#Low_complexity
Seq_primer: M13 Forward
POLYA=Yes.
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1514 CTCTGGTTGGTTGTAGTGGTGATCAGGAAACAGATCTCTCAGCAAAGCCACTGAGGAGGAGG
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cDNA clone PLACE1009110 5', mRNA
/mol_type="mmm" or property of the property of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           529 AAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAAGATACAATCAAAATCCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCTGGTCTCTATTCCCATGAAAAAGTGCTCATGACATATTGAGAAGACCTACTTACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   469 IGCIGGICTCIAITCCCAIGAAAAGIGCICAIGACAIAITGAGAAGACCIACTIACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                                                     21.5%; Score 551.4; DB 5;
87.0%; Pred. No. 3.6e-131;
ive 0; Mismatches 91;
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Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30383465.
Contact: Genoscope
Contact: Genoscope - Centre National de Sequencage
Z rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAI018ZD02_CS01644_2&c=1383.f
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BX350083 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA CODO 25-NORMALIZED Homo sapiens CDNA CLONE CSODI013YA07 3-PRIME, mRNA sequence.
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Catarrhini; Hominidae; Homo.
          ATGCCAGCCTGTCCCCGTCATCCTGGGTGTCCAGGGTGGAAGCCAGTGCCTGTCATGTG
                                                                                                                                                   GGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGAGAGCTCTATCTTG
                                                                                                                                                                                                                                                                                                                                                                                         TCGAGTCGGCTGCCTGCCCGGGCTGCTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATCACTCTTTCTGCTCTCAGGACCCC
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                                                                                                               GGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG
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                                                                                                                                                                                                                                                    GTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGGACATGGGGCTCACCTCCAGCT
                                                                                                                                                                                                                                                                                           GTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGGACATGGGGCTCACCTCCAGCT
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Mammalia, Eutheria, Primates,
1 (bases 1 to 915)
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1. .915
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BX350083.2
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1273

1333

290

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1453

EST

ACCESSION KEYWORDS

VERSION

ORGANISM

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

170

230

1513

110

20

1383.£

FEATURES

1034

1093

530

1153

1213

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1. .555
/ organism="Homo sapiens"
/mol_type="mRNA"
/db xref="Laxon:966"
/dev_stage="Adult"
/dov_stage="Adult"
/dov_stage="Adult"
/dov_stage="Adult"
/clone lib="HT0773"
/note="Organ: head neck; Vector: puc18; Site_1: SmaI;
/note="Organ: head neck; Vector: puc18; Site_1: SmaI;
/site_2: SmaI; A mini-library was made by cloning products
/derived from ORESTES PCR (U.S. Letters Patent application
/no. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 555)
Dias Neto,E., Garcia Corra,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., Go'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                              BQ351235 555 bp mRNA linear EST 20-MAY-2002 RC0-HT0773-010600-021-e07 HT0773 Homo Sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCO&t2=RCO-HT0773-
010600-021-e07&t2=2000-06-01&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence start: 14
High quality sequence stop: 555.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1851 CTGGTTTCCTTGTATGAAAGGAGAGACACAGAGACAGAGAGACGCGGGGAAGACTAT 1910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1792 AGAIGIAGITAGITAAGACAAGGICAIGCIGGAIGAAGGIAGACC-TAAAITCAATAIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 AGATATAGTGAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCGTAAATTCAATATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.8%; Score 481; DB 5; Length 55 98.6%; Pred. No. 5.5e-113; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                          BQ351235.1 GI:21015291
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              695 ACTGGATGGTGCTACTGCTGTGGAACCTTGTAAAAACCATGTGGGGTAAACTGGGAATAA 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATGAAAAGATTTCTGTGGGGGTGGGGTGGGGGAGTGCTGGGAATCATTCCTGCTTAATG 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GTAACTGACAAGTGTTACCCTGAGCCCCGCAGGCCAACCCATCCCCAGTTGAGCCTTACA 180
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                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 555)
                                                                                                                                                                                                                                                                                                                                                                                             Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute
                                                                                                                          Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTGGATGGTGCTACTGCTGTGGGAACCTTGTAAAAACCATGTGGGTAAACTGGGAATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTCAGTAGCTCTCCACATGAAGTCCTCTCACTACCACTGTGCAGGAGAGGAGGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.6%; Score 527.8; DB 1; Length 555; 97.8%; Pred. No. 4.1e-125; ive 0; Mismatches 11; Indels 1
                                                                                                                                                                                                                                                                                            Helix Research Institute
1153-2-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="placenta"
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/note="Vector: pME18SFL3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                              HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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(Daaes 1 to 468)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Grodd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Warg, G., Scheng, X.H., White, T.J., Sninsky, J.J., Adame, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inferring nonneutral evolution from human-chimp-mouse orthologous
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                                                GATAACGGCTCTGCTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAT
                                                                                                                                                                                                                                                                                 447 AATGTACCAAAGTTGTCTTTGTGA-CCAATAGAATATGGCAGAAGTGATGGCATGCCCCT
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/locus_tag="HCM4832"
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1 ATGGTCCTGAGTGGGGGGGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTAT
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ALIGNMENTS

Human; IL-IL1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis; chromosome 2q13; inflammatory disease; heart disease; Graves' disease; rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer; osteoporosis; systemic lupus erythematosus; ss. Human IL-IL1 coding sequence 5' end #1. BP. AAF27922 standard; cDNA; 39 (first entry) 08-MAY-2001 AAF27922; AAF2792:

Homo sapiens.

WO200105974-A2

25-JAN-2001.

17-JUL-2000; 2000WO-US019508.

99US-0144298P 16-JUL-1999; (INTE-) INTERLEUKIN GENETICS INC.

Nicklin M, Barton J;

WPI; 2001-091974/10.

Nucleic acids encoding human and murine interleukin-1L1 polypeptides useful for controlling inflammatory processes.

Claim 20; Fig 1; 150pp; English.

The present invention provides the protein and coding sequences of the human and murine interleukin-ILI (IL-ILI) proteins. The IL-ILI gene is located between the IL-lbeta and IL-Ireceptor genes at human chromosome 2q13. The sequences are useful in the diagnosis, prevention and treatment of heart disease, cancer and inflammatory diseases such as rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disorder, diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,

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The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jackman J, Schoenfeld J, Williams PM,
                                                                                                                                                                             ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
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Pred. No. 0.0004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1437; 3069pp; English
                  ADN05043 standard; cDNA; 2720 BP.
                                                                                                                                        Antipsoriatic cDNA sequence #737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.9%;
                                                                                                                                                                                                                                                                                                                                          25-SEP-2003; 2003WO-US030907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF31355 standard; DNA; 5751
                                                                                                                                                                                                                                                                                                                                                                                 25-SEP-2002; 2002US-0414006P.
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic clone B2HFLS20W.
                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Lang 38; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-305105/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; ADN05044
                                                                                                                                                                                                                                                              WO2004028479-A2.
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                                                                                                                                                                                                                         Homo sapiens.
                                                                                                 01-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bodary S,
                                                           ADN05043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF31355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ношо
ADN05043
ID ADNO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; IL-IL1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis; chromosome 2q13; inflammatory disease; heart disease; Graves' disease; rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;
severe periodontal disease and pregnancy complications. The present sequence is one of two alternative 5' ends of the human IL-IL1 coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding human and murine interleukin-11, polypeptides
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                                                                                                                       Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                             0; Indels
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                                                                              Seguence 39 BP; 12 A; 12 C; 11 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA 39
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                                                                                                                                                                                                                             1 TTGAGGAACAGGCAGACTCCCACAGCTCCCGCCAGGAGAA 39
                                                                                                                                                                                                      TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA
                                                                                                                                          Pred. No. 6.7e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for controlling inflammatory processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is an IL-IL1 coding sequence fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 osteoporosis; systemic lupus erythematosus; ds
                                                                                                                   100.0%; Score 39; DB
100.0%; Pred. No. 6.7e
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interleukin-IL1 coding sequence fragment #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INTE-) INTERLEUKIN GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Fig 10; 150pp; English
                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-2000; 2000WO-US019508
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1 Similarity 97.4%;
38; Conservative
                                                                                                                                                                                                                                                                                                                                              54
                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-2001 (first entry)
                                                                                                                                        Best Local Similarity 100.
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                              AAF27927 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barton J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-091974/10.
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Matches 38; Conser
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                                                                                                                                                                                                                                                                                                                                                                                      AAF27927;
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Wood WI;

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interleukin; IL-1 receptor; cancer; inflammation; ds.
83 TGGAGGAACAGGCAGACTCCCACCCCCGCCAGGAGAA 121
                                                                                                                                      07-JUL-2000; 2000WO-US018710.
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RESULT 3

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Gaps

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1; Indels

DB 12; Length 2720;

Ford J,

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High inhibitors are used in the method of the invention. The specification describes a method of inhibiting B-cell proliferation, activation or differentiation. The method comprises administering an activation or differentiation. The method comprises administering an inhibitor of IL-1My1 activity to a human with alevated B-cell levels or activity, in an amount that inhibiting B-cell proliferation induced by IL-1My1. The method is useful for inhibiting or stimulating B-cell proliferation, activation or differentiation in patients having a B-cell-related disorder (e.g. lymphoma, leukemia, myeloma or infection) or an autoimmune disease (e.g. allergy, asthma or allergy crhinitis), or in polypeptide, or the inhibitor of IL-1My1 activity, is useful in preparing a medicament for stimulating or reducing B-cell differentiation. The IL-1HY1 differentiation or activation. The IL-1HY1 polypeptide may also be used in preparing a medicament for reducing IgA production
                        present sequence encodes human interleukin (IL)-1Hyl polypeptide. IL-
inhihitors are used in the method of the invention. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; interleukin-1 receptor; IL-1; antagonist; sepsis; acute pancreatitis; endotoxic shock; cytokine induced shock; rheumatoid arthritis; chronic inflammatory arthritis; pancreatic cell damage; diabetes mellitus type 1; pancreatic cell damage; diabetes mellitus type 1; pulmonary disease; inflammatory bowel disease; inflammation; pulmonary disease; autoimmune disease; inflammatory disease; antiproliferative; myelogenous leukemia; premature labor; intrauterine infection; nutritional activity; activity; activity; activity; activity; activity; activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemokinetic activity; hemostatic activity; thrombolytic activity;
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5751 BP; 1466 A; 1274 C; 1489 G; 1383 T; 0 U; 139 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Length 5751;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding a human interleukin-1 receptor antagonist
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D, Kita D, Ford J, Pace A, Alfenito M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          813 recadedacadecadacrecadaderecedecadada 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 95.9%; Score 37.4; DB 8; Local Similarity 97.4%; Pred. No. 0.00043; Nes 38; Conservative 0; Mismatches 1
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98US-00079909.
98US-00092364.
98US-00127698.
99US-00229591.
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17-FEB-1999;
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Matches
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                                                                                                                                                                                                                                                          Isolated nucleic acids encoding interleukin-1 (IL-1) receptor antagonist proteins (referred as IL-1Hy1), useful in the treatment of cancer, e.g. breast adenocarcinoma and brain tumors, and an inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins. IL-1Hyl is useful for treating cancer, an inflammatory disease mediated by IL-1B, inflammation resulting from infection or allergic reactions, and inflammation associated with chronic bronchitis, arthritis, diabetes or endothermia
                                                                                                                                                                                                                                                                                                                                                                                                                            present invention relates to interleukin (IL)-1 receptor antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5751 BP; 1466 A; 1274 C; 1489 G; 1383 T; 0 U; 139 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting or stimulating B-cell proliferation, activation or differentiation, useful for treating B-cell-related disorders or autoimmune diseases, comprises administering an interleukin-1Hyl polypeptide or its inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.9%; Score 37.4; DB 4; Length 5751; 97.4%; Pred, No. 0.00043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic DNA sequence of a human Interleukin-1Hy1 (IL-1Hy1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGAGGAACAGGCAGACTCCACAGGCTCCCGCCAGGAGAA 851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 9; 179pp; English.
13-OCT-1999; 99US-00417455.
08-DEC-1999; 99US-00457626.
08-DEC-2090; 2000US-00523552.
22-MAY-2000; 2000US-00576008.
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29-NOV-2001; 2001US-0334668P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 97.4 nes 38; Conservative
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                                                                                                                                                                                                                WPI; 2001-071582/08
                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                     mediated by IL-18.
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                                                                                                                                                                Pace A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003010291-A2
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Nucleic acids encoding human and murine interleukin-1L1 polypeptides useful for controlling inflammatory processes.
                                                                                                                                                                                                                                       (INTE-) INTERLEUKIN GENETICS INC
                                                                                                                                                                                                                                                                        Example; Fig 11; 150pp; English
                                                                                                                                                                                                                                              Nicklin M, Barton J;
                                                                                                                                                                                                                                                     WPI; 2001-091974/10.
                                                                                                                                                                                                         WO200105974-A2.
                                                                                                                                                                                                                                16-JUL-1999;
                                                                                                                                                                08-MAY-2001
                                                                                                                                                                                                                 25-JAN-2001
                                                                                                                                                         AAF27950;
                                                                                                                                         g
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inflammatory processes.

The present invention provides the protein and coding sequences of the Homo sapiens WO9951744-A2 05-APR-1999; 17-FEB-1999; 26-JAN-2000 .5-MAY-1998; 03-APR-1998; 11-JUL-1998; 14-OCT-1999 9-JUN-1998 20-MAY-1998 .3-JAN-1999 AAZ30053; RESULT 8 AAZ30053 g 888888888888888 ò The present sequence encouse a numan interieudant, itd., itd .. 0 New isolated interleukin-1 receptor binding polypeptides, used to treat e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease, inflammatory disease, autoimmune disease or proliferative disease. Human, IL-ILI; interleukin-1 locus; IL-lbeta; IL-lreceptor; psoriasis; chromosone 2q13; inflammatory disease; heart disease; Graves' disease; wheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer; osteoporosis; systemic lupus erythematosus; ds. Gape present sequence encodes a human interleukin-1 (IL-1) receptor Sequence 5752 BP; 1467 A; 1274 C; 1489 G; 1383 T; 0 U; 139 Other; 0, Length 5752; can also be used for detection, diagnosis and drug screening 1; Indels 813 TGGAGGAACAGGCAGACTCCCACAGCTCCCGCCAGGAGAA 851 1 TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA 39 Query Match

95.9%; Score 37.4; DB 2;
Best Local Similarity 97.4%; Pred. No. 0.00043;
Matches 38; Conservative 0; Mismatches 1: Claim 1; Fig 9A-C; 123pp; English. Interleukin-IL1 genomic sequence. AAF27950 standard; DNA; 6540 17-JUL-2000; 2000WO-US019508 99US-0144298P (first entry)

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human and murine interfeukin-ILI (IL-ILI) proteins. The IL-ILI gene is located between the IL-lbeta and IL-lreceptor genes at human chromosome 2413. The sequences are useful in the diagnosis, prevention and treatment of heart disease, cancer and inflammatory diseases such as rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disorder, diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated interleukin-1 receptor binding polypeptides, used to treat e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease, inflammatory disease, autoimmune disease or proliferative disease.
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; interleukin-1 receptor; IL-1; antagonist; sepsis; acute pancreatitis; endotoxic shock; cytokine induced shock; rheumatoid arthritis; chronic inflammatory arthritis; pancreatic cell damage; diabetes mellitus type 1; graft versus host disease; inflammatory bowel disease; inflammatory bowel disease; antimmune disease; inflammatory disease; antimmune disease; inflammatory disease; antimmune disease; inflammatory disease; intrauterine infection; nutritional activity; hematopoiseis regulating activity; tissue growth activity; activity; inhibin activity; chemotactic activity; anti-inflammatory activity; se.
                                                                                                                  severe periodontal disease and pregnancy complications. The present sequence is the IL-IL1 gene
                                                                                                                                                                          Sequence 6540 BP; 1747 A; 1458 C; 1709 G; 1626 T; 0 U; 0 Other;
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                                                                                                                                                                                                                   Length 6540;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding a human interleukin-1 receptor antagonist.
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Ford J, Pace A, Alfenito M;
                                                                                                                                                                                                                                                                                                                                  970 TGGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA 1008
                                                                                                                                                                                                                                                                                             39
                                                                                                                                                                                                                                                                                             1 TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA
                                                                                                                                                                                                               Score 37.4; DB 5;
Pred. No. 0.00044;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                               BP
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                                                                                                                                                                                                               Query Match 95.9%;
Best Local Similarity 97.4%;
Matches 38; Conservative (
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Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-611042/52
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Sequence 7605 BP; 2079 A; 1647 C; 1865 G; 2009 T; 0 U; 5 Other;

arthritis, diabetes or endothermia

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The present sequence encodes a human interleukin-1 (IL-1) receptor antagonist. It is an extension of AA23052. The encoded polypeptide is capable of binding IL-1 receptors (IL-1RS). The polymucleotides and polypeptides can be used for the prevention or treatment of disorders involving sepsis, acute pancreatitis, endotoxic shock, cytokine induced shock, rheumatorid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammatory powel disease, inflammatory disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia antiproliferative agent such as for acute or chronic myelogenous cor in the prevention of premature labor secondary to intrauterine infections. They can also exhibit activities such as e.g. nutritional activity, cytokine and cell proliferation/differentiation activity, chemotactic/ chemokinetic activity, hemostatic and thrombolytic activity, receptor/ chemokinetic activity, hemostatic and thrombolytic activity, receptor/ ligand activity, and also be dispersed and activity of activity, receptor/ contents and activity activity. The products can also be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acids encoding interleukin-1 (IL-1) receptor antagonist proteins (referred as IL-1Hy1), useful in the treatment of cancer, e.g. breast adenocarcinoma and brain tumors, and an inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                 Sequence 7605 BP; 2081 A; 1647 C; 1865 G; 2007 T; 0 U; 5 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interleukin; IL-1 receptor; cancer; inflammation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            39
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA
                                                                                                                                                                                                                                                                                                             used for detection, diagnosis and drug screening
                                                                                                                                                                                                                                                                                                                                                                                     Score 37.4; DB 2;
Pred. No. 0.00044;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extension of genomic clone B2HFLS20W
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99US-00417455.
99US-00457626.
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                                                                                                                                                                                                                                                                                                                                                                                     Match 95.9%;
Local Similarity 97.4%;
es 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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The present invention relates to interleukin (IL)-1 receptor antagonist proteins. IL-1Hyl is useful for treating cancer, an inflammatory disease mediated by IL-18, inflammation resulting from infection or allergic reactions, and inflammation associated with chronic bronchitis,

Disclosure, Fig 10; 179pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     differentiation or activation. The IL-1HY1 polypeptide may also be used in preparing a medicament for reducing IgA production
                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                               Interleukin-1Hy1; IL-1Hy1; B-cell proliferation; B-cell activation; B-cell differentiation; B-cell-related disorder; lymphoma; leukemia; meyeloma; infection; autoimmune disease; allergy; asthma; allergic rhinitis; IgA production; ss.
                                                                                                                                                                                                                                                                                                                              Extended genomic DNA sequence of a human Interleukin-1Hy1 (IL-1Hy1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting or stimulating B-cell proliferation, activation or differentiation, useful for treating B-cell-related disorders or autoimmune diseases, comprises administering an interleukin-1Hyl polypeptide or its inhibitor.
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 Length 7605;
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Pred. No. 0.00044;
0; Mismatches 1; Indels 0
                                     Indels
                                                                                                 1838 TGGAGGAACAGGCAGACTCCACAGGCTCCCGCCAGGAGAA 1876
                                                                           1 TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA 39
   4
Score 37.4; DB 4;
Pred. No. 0.00044;
0; Mismatches 1
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                                                                                                                                                                                                            ABZ77451 standard; cDNA; 7605
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29-NOV-2001; 2001US-0334668P.
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Best Local Similarity 97.4%;
Matches 38; Conservative
Query Match
Best Local Similarity 97.4%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                      28-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin H, Ford JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-239438/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                        RESULT 10
ABZ77451
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The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening of bioactive agent capable of binding drug candidates; (ii) for screening of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for reating; (x) for diagnosing carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma as Sasociated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                            Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 967; Opp; English
                                                                                                                                                                                                                                                                     28-FEB-2003; 2003WO-US006235.
                                                                                                                                                                                                                                                                                                                                 01-MAR-2002; 2002US-00087192.
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                                                                                                                                                  WO2003073826-A2.
                                                                                       Mus musculus.
                                                                                                                                                                                                             12-SEP-2003
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AAK61778/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genomic polynucleotide SEQ ID NO 30715.
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                            1 TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA 39
1838 TGGAGGAACAGGCAGAGCTCCCAGGAGAA 1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22.8; DB 4;
Pred. No. 1.1e+02;
0; Mismatches 7;
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11-JUL-2000; 2000US-00614150
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Best Local Similarity 79.4%;
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
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                           Sequence 49087 BP; 13649 A; 10829 C; 11010 G; 13318 T; 0 U; 281 Other;
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                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                 Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:6838.
                                                      Score 22.6; DB 11; Length 49087;
Pred. No. 1.7e+02;
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US2002182586A1, for which no sequence data was published
                                                                                                                                                      41121 Trgaggaacagacagacacgaaacrrrccrcraggag 41085
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                                                                                                                         1 TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAG 37
                                                                                          0; Mismatches
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                                                         Query Match 57.9%;
Best Local Similarity 75.7%;
Matches 28; Conservative (
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Gaps

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Indels

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RESULT 12 ACN44492/c

Mouse genomic sequence mCG20206.

18-NOV-2004

ACN44492

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2000US - 02599P. (HUMA-) HUMAN GENOME SCI 02-OCT-2000)
13-OCT-2000)
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20-OCT-2000)
20-OC 11-DEC-2000;

S Ruben Rosen CA, Barash SC,

WPI; 2001-483426/52 P-PSDB; AAM88997.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Claim 1; SEQ ID NO 6838; 3071pp + Sequence Listing; English.

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
co supplement the patients own production of (I). Additionally, (I)
co polynucleotides may be used to produce the secreted (I), by inserting the
nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-derived cells. AAK64703
concers and cancer metastases of haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54912 to AAK64950 and AAM82169
crepresent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlbS; ds; acquired immune deficiency syndrome.
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11-JUL-2000; 2000US-0217487P.
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Claim 1; SEQ ID NO 1403; 880pp; English.
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05-JAN-2001; 2001US-0259678P
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The invention relates to novel isolated polypeptides (I), and polynucleotides (II). (I) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (sickle cell anaemia), myeloproliferative disorders, blaschers, primary hemmatopoietic disorders, hyperproliferative disorders (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal abnormalities Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.

14-AUG-2000;

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(Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders, in wound healing, epithelial cell proliferation, endocrine disorders (e.g. Addison's disease), reproductive system disorders, gastrointestinal disorders (inflammatory disorders), liver disorders (cirrhosis), as stimulators of b-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS25976-AAS27850 represent novel signal transduction pathway protein coding sequences and PCR primers of the invention
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81.2%; Pred. No. 1.7e+02;
tive 0; Mismatches 6; Indels 0;
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nes 26; Conservative
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure, SEQ ID NO 36975; 3071pp + Sequence Listing; English.

AMX54951 to AAX64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM8110 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome concerns the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the patients and polynucleotides may be used to provent, characterism and polynucleotides may be used to provent, characterism and polynucleotides may be used to prevent, characterism and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, characterism and concern and cancer metastases of haematopoietic-related diseases, especially concerns and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK84992 to AAK84950 and AAM82169 represent invention

Sequence 7667 BP; 1430 A; 2150 C; 2370 G; 1717 T; 0 U; 0 Other;

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Query Match

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